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Listing first 45 summaries
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ABP61910
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2301.535 Million cell updates/sec
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Human protein #2 u
Human protein
Human p63 protein
Human oncogene p58
Human oncogene p59
Human oncogene p51
Human lung cancer
                                                                                                                                                                                                          Description
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lung cancer
p53 homologu
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AAB82128 ABG95127	AAB11359	AAY05955	AAY05963	ABB74994	ABP61914	ABG95138	ABG95131	AAB11362	ABG95134	ABG95129	ABB74995	ABP61915	ABG95141	ABG95135 ·	AAB11363	AAY05954	AAY05962	ABB74949	ABP61869	AAB11317	AAY41032	ABB74989	ABP61909	AAB11357	ABG95132	ABG95140	AAY05956	AAY50998	AAY05958	ABB74993	ABP61913	9	AAB11361
	p63 protein	Himan cell requiat	cell	p53 h	lung	oncogene	oncogene	p6:	ono	onc	p53 h	lur	oncogene p6	onco	p63 protein	cell regula	cell	lung	lung	lung cancer	lung	p53 homolo	lung	p63 prote	oncogene p5	oncogene p6	an ce	KET pro	cell	p53 h	lung	KET prote	Human p63 protein

ALIGNMENTS

AAY45247;

AAY45247 standard; Protein;

641 AA.

RESULT 1
AAX'45247
ID AAX'4
XX AAX'4
CT O7-J
DE Huma
XX Huma
XX Huma
XX Huma
XX Homo
X Key Domain 07-OCT-1999. Domain Human; p51; p53 related gene; cell proliferation; regulation; cancer; tumour suppression; diagnosis. (SAKA) OTSUKA PHARM CO LTD 27-MAR-1998; 24-MAR-1999; W09950412-A1 Domain Homo sapiens Human p51 protein B. 07-JAN-2000 (first entry) 98JP-0100467 99WO-JP01512 142..321 /label= DNA_binding_domain 353..397 /label= oligomerisation_domain Location/Qualifiers /label= transactivation_domain

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Best Local S
Matches 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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DB; AAZ25771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVI 600
                                                                                                            SPTQALPPPLSMPSTSHCTPPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHY
                                                                                                                                                            GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                                                                                                                                                          FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
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DAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                       DAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 641
                                                                                              SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHY
                                                                                                                                              GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                                                                                                             LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                                                                                           LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                          DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                               SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVI
                                                                                                                                                                                                                                                                                                                                           PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 152-154; 163pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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creening for
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Pred. No. 2.4e-273;
Mismatches 0;
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CC cell regulatory proteins (CRPs) termed the p63 family of cell regulatory proteins (CRPs) termed the p63 family of proteins, CC which demonstrate certain sequence identity to known tumour CC which demonstrate certain sequence identity to known tumour CC suppressor proteins p53 and p73. It has been observed that the CC intron-exon organisation is conserved between p73 and p53, and from CC known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy CC of amplifying 2 exons in a conserved domain and their intervening CC intron. The human p53 gene was localised to chromosomal position CC 3q27-29. At least 6 different isotypes exist. Splice variants are CC differing at the C-terminus have been designated as alpha, beta and CC gamma forms, while p63 members differing in the N-terminus are CC designated as deltaN and TA forms, where the deltaN form lacks the CC transactivation domain. The present sequence represents human CC p63 isotype TAp63 alpha. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent CC activities, such as the ability to transactivate p53 reporter genes CC and induce apoptosis. Cessation or down-regulation of p63 expression CC may play a critical role in the process of cervical squamous CC differentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. CC acchexia) and neuronal differentiation and related degenerative CC disorders. p63 polypeptides (see AAV05953-64), polynucleotides (see CAX58572-83) and anti-p63 antibodies of the invention can be used to CC identify compounds useful for treating disorders involving such CC identify compounds useful for treating disorders involving such CC identify compounds and anti-p63 antibodies of the invention can be used to CC identify compounds and compounds and diagnosis, and in the production of
Query Match
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                                                                           Sequence
                                                                                                              processes,
transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 23; Fig 9; 161pp; English.
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15-OCT-1997;
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cancer; tumour suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated p63 cell regulatory protein for, e.g. treatment
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                   Local Similarity
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                                                                                                                                  detection and diagnosis,
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97US-0062076.
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Score 3405; DB 20;
Pred. No. 2.4e-273;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimera gene of the p53 family, useful for gene of cancer, comprises a transcription activating binding region -
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                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
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                                                                                                                                 641;
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61 DSDLSDPMWPQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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                                                                                                                                                  Similarity
                                                             MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                        {\tt MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ}
                                                                                                                                                                                                              641 AA;
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                                                                                                                             Conservative
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                                                                                                                                                                                                                                                  is the amino acid sequence of a human oncogenic protein
                                                                                                                                              100.0%;
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                                                                                                                                            Score 3405; DB 23;
Pred. No. 2.4e-273;
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
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2000US-0510376
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99US-0466396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunogenic; cytostatic;
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N-PSDB; AAC66028

Matches Query Match Best Local (

61 19

shock protein 90;

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This invention describes a novel isolated polypeptide (1) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient cells expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 development of cancer.
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Pred. No. 5.1e-273;
0; Mismatches 1;
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                                                                                                                                                                                                                                                    CC protein (HSD)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p33), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC protein isoform yeloid leukaemia (CML), APL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                   Matches
                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein or cellular protein isoforms (II) dependent on heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
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)B; ABS73328.
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99.8%;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                               synovial sarcoma; viral infection
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cc associated with chromosomal aberrations yielding oncogenic fusion ccell population, treating cancerous cells containing (I) in a heterogeneous ccell population, treating proliferative diseases associated with mutant crotein or cellular protein isoforms (II) dependent on heat shock containing (Byp)-90, or selectively treating cells expressing (II) containing (II) and containing (II) containing (II) containing (II) containing (II) containing (II) containing distribution isoform containing cells expressing (II) concogenic fusion protein, treating cancerous cells containing fusion concogenic fusion protein isoform dependent on heat shock protein (HSP)-90 (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful containing a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemaia (CMI), AFL, AKL, AKL, NHL and CMML, contained a sarcoma, chronic myeloid leukaemaia (CMI), AFL, ALL, AKL, NHL and CMML, contained a sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and contained containe Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90 describes a method of treating 338-340; English. genetically-defined disease

Query Match Best Local S Matches 640 Sequence Local Similarity 640; 641 AA; Conservative 99.98; Score 3401; DB 23; Pred. No. 5.1e-273; 0; Mismatches 1; Indels Length 641; 0 Gaps

ő 밁 Š В Ş В δÃ В δÃ 밁 δõ 밁 δõ В δÃ 밁 Qy 멍 δô 121 241 241 181 121 421 421 361 361 301 301 181 61 61 MSOSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSPYAQPSSTFDAL MSQSTQTNEFLSPEVFQHIMDFLEQPICSVQPIDLNEVDEPSEDGATNKIEISMDCIRMQ PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 120 180 180 120 60 600 480 480 420 420 360 360 300 300 240 240 600 540

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                CC The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic CC activity, and can be used in gene therapy and in vaccines. Compositions CC comprising (I) or (II) can be used for stimulating an immune response in CC a patient and for treating lung cancer in a patient. Oligonucleotides of C (I) can be used for detecting the presence of a cancer in a patient, by Obtaining a biological sample from the patient, contacting the CC biological sample with the oligonucleotide, detecting in the sample, an CC amount of polynucleotide that hybridises to the oligonucleotide and CC comparing the amount of polynucleotide that hybridises to the CC oligonucleotide to a predetermined cut-off value, and determining the CC presence of a cancer in the patient. (I) and (II) are useful in CC presence of a cancer in the patient. (I) and (II) are useful as a marker to CC indicate the presence or absence of a cancer such as lung cancer. CC ABQ92145 to ABQ92486 and ABP61866 to ABP6192 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                   Query Match
Best Local S
Matches 640
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McNeill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-2000; 2000US-0735705
07-MAY-2001; 2001US-0850716
28-JUN-2001; 2001US-0897778
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PD, Fanger N, Rette
, Watanabe Y, Peckh
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                        DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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                                                                                                                                                                                                         99.98;
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Retter MW, Durham M, Fanger GR,
Peckham DW, Cai F, Foy TM;
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                                                                                                                                                                                   0;
                                                                                                                                                                                Score 3401; DB 23;
Pred. No. 5.1e-273;
0; Mismatches 1;
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                                                                                                                                                  28-JUN-2000;
02-AUG-2000;
21-AUG-2000;
15-SEP-2000;
09-OCT-2000;
12-DEC-2000;
07-MAY-2001;
                     Wang T, Wang A, Skeil
McNeill PD, Fanger N,
                                                                                                 (CORI-)
                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2001;
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2000US-0630940.
2000US-0643597.
2000US-0662786.
2000US-0685696.
2000US-0735705.
2001US-0850716.
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                     Skeiky YAW, Li
er N, Retter MW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; cytostatic; immunostimulant; vaccine;
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W, Marnerakis
                Kalos MD,
                     Henderson RA;
Fanger GR;
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Best Local Sim.
Matches 640;
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This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypuncleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 250-253;
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ine; detection.
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             This invention describes a novel KET-encoding nucleic acid (I) and its fragments, variants and mutants which has anticancer activity. (I) encodes a protein, (II), involved in control of the cell cycle and apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to detect (I) in biological samples, specifically anglogenic tumor tissue, including (I) sequences that have a homozygotic deletion and (b) to detect presence or absence of human chromosome 3q27 or murine chromosome 16, or their fragments, by hybridization. Also, (I) is used as a tumor tissue, and the presence of human chromosome 3q27 or murine chromosome 16, or their fragments, by hybridization. Also, (I) is used as a tumor
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                                                            SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVI
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                                               SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVI
                                                                                                  SPTQALPPPLSMPSTSQCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHY
                                                                                                                                                  GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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Pred. No. 1.2e
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ABP61913 standard; Protein; 680 8

ABP61913;

07-OCT-2002 (first entry)

Human lung cancer associated protein sequence SEQ IJ NO:342

Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine

Homo sapiens

WO200247534-A2

20-JUN-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes isolated human lung carcinoma compositions polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the containing a biological sample from the patient, contacting the anamount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the coligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to confident the presence or absence of a cancer such as lung cancer.

Chalcate the presence or absence of a cancer such as lung cancer.

Chalcate the presence or absence of a cancer such as lung cancer.

Chalcate the presence or absence of a cancer such as lung cancer.
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Best Local S
Matches 640
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McNeill PD,
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07-MAY-2001;
28-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer -
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PD, Fanger
), Watanabe
FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
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                                                                                                                                       ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
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; 2001US-0850716.
; 2001US-0897778.
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er N, Retter MW,
be Y, Peckham DW,
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, Durham M, Fanger
W, Cai F, Foy TM;
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L.2e-272;
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RESULT 13
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02-AUG-2000;
21-AUG-2000;
15-SEP-2000;
09-OCT-2000;
                                                            The present invention describes human lung tumour proteins. Human lun tumour proteins and polynucleotides have cytostatic and immunostimula activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, Teall populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer stimulating an immune response. ABL4930 to ABL4930 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang T,
McNeill
  Sequence
                                                                                                                                                                                                                                                                                                                            Polynucleotides encoding lung cancer or stimulating
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07-MAY-2001;
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2000US-0630940.
; 2000US-0643597.
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', Marnerakis M,
Y, Peckham DW;
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15-OCT-1997;
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                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                   Cell regulatory protein; p63; hu-deltaNp63 gamma; human;
                                                                                                                                                                                                                                                                                                                                           Human cell regulatory protein
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oliferation; cell differentiation; thera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHY
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                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                          98US-0087216.
97US-0062076.
                                                                                        98WO-US21992
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                                                                                                                                                                                                                                                                             apoptosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          introm. The human p53 gene was localised to chromosomal position 32 3q27-29. At least 6 different isotypes exist. Splice variants and 3q27-29. At least 6 different isotypes exist. Splice variants of differing at the C-terminus have been designated as alpha, beta and 3q27-29. At least 6 differing in the N-terminus are designated as deltaN and TA forms, where the deltaN form lacks the transactivation domain. The present's equence represents human 3c p63 isotype hu-deltaNp63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous afferentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. C achexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AN705953-64), polynucleotides (see AN705953-64), polynucleotides (see C ANX5872-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McKeon F,
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LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLLQKQTSIQSPSSY
                                                                                                                                                                                                                                MSQSTQTNEELSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                        FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                      ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
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                                                                FEARICACPGRDRKADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
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98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 3353; DB 20;
Pred. No. 5.3e-269;
8; Mismatches 4;
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                                                                             This invention describes a novel KET-encoding nucleic acid (I) and its fragments, variants and mutants which has anticancer activity. (I) encodes a protein, (II), involved in control of the cell cycle and apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to detect (II) in biological samples, specifically angiogenic tumor tissue, including (I) sequences that have a homozygotic deletion and (b) to detect presence or absence of human chromosome 3q27 or murine chromosome 16, or their fragments, by hybridization. Also, (I) is used as a tumor suppressor, particularly in tumors where an alteration in the wild-type p53 allele has not been identified. (I) and (II) may also be used for development of specific cytotoxic agents and for predicting the risk of developing cancer. This sequence represents the rat KET protein described in the mathem acts the invention.
                                                Sequence
                                                                                                                                                                                                                                                       Disclosure; Fig 1; 28pp; German.
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Search completed: August Job time: 46.2069 secs 7,

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455011
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SED ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
TYPE: PRT
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Homo sapiens
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Fanger, Gary R
Li, Samuel X.
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Fan, Liqun
Kalos, Michael D.
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US-08-390-515C-7
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Scoring table:

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APPLICANT: KAIOS, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANTIFLE OF INVENTION: AND DIAGNOSIS OF LUNG CANTIFLE OF INVENTION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
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Matches 640;
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APPLICANT: Fan, Liqun
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                                         PQGAVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                    SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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                            PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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Pred. No. 2.9e
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Matches
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 339
LENGTH: 641
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APPLICANT:
APPLICANT:
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APPLICANT: Wang, Aljun

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C9

CURRENT APPLICATION NUMBER: US/09/606,421B

CURRENT FILING DATE: 2000-06-28
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les 640; Conserv
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PQGAVIRAMPYYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                         SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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Pred. No. 2.9e-304;
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CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.C
SEQ ID NO 342
LENGTH: 680
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                                                                                                                                                                                            LENGTH: 680
TYPE: PRT
ORGANISM: Homo sapiens
-09-643-597-342
                                                                                                                                                                                                                                                                                                             APPLICANT: MCNEILL, PATTICIA D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
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                          Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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Best Local
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                                                                                                                                      Matches
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APPLICANT: Hasken, Nancy A.
APPLICANT: Fanger, Garty R.
TITLE OF INVENTION: COMPOUNDS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
FILE REFERENCE: Z10121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
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                                                                                              1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                 Similarity.
                          DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                          DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
                                                                                MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Fan, Liqun
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                                                                                                                                   Score 3397; DB 4;
Pred. No. 7.4e-304;
0; Mismatches 1;
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OF LUNG CANCER
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APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FRACESC for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
TYDE: PRT
ORGANISM: Homo sapiens
US-09-606-421B-342
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Best Local S
Matches 640
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o. 6531315
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                                                                                                         Similarity
DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPVNTDHAQNSVTAPSPYAQPSSTFDAL
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Fanger, Gary R.
Li, Samuel X.
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Bangur, Chaitanya
                                                                                            Conservative
                                                                                                      99.8%;
                                                                                          Score 3397; D
Pred. No. 7.4e
0; Mismatches
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7.4e-304;
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US-09-643-597-338
                                                                                                                 NUMBER OF SEQ ID NOS: 369
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 338
LENGTH: 586
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 338,
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APPLICANT: McNeill, Patticia D.
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: AND DIAGNOSIS OF
FILE REFERENCE: 210121.455C11
                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                          CURRENT FILING DATE: 2000-08-21 NUMBER OF SEQ ID NOS: 369
                                                                                                                                                                                 CURRENT APPLICATION NUMBER:
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                                       Similarity
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 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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Fan, Liqun
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                         Score 3016; Di
Pred. No. 6.9e
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FC
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
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US-09-542-615A-338
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APPLICANT: Wang, To
                                                                                                         Best
                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 338, Application Patent No. 6518256
                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
09-542-615A-338
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                                                                                           Conservative
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                                                                                        Score 3016; DB 4;
Pred. No. 6.9e-269;
1; Mismatches 2;
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitan
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 338
LENGTH: 586
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                                                                                                       Matches
                                                                                                                    Query Match
Best Local :
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.45509
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
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                                                                          PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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Fanger, Gary R.
Li, Samuel X.
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APPLICANT: Skekky, Yasir A.W.
APPLICANT: Skekky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeili, Patricia D.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS 369
SOFTWARE: FastSEQ for Window
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
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; TYPE: PRT
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Pred. No. 3e-268;
2; Mismatches
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APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
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US-09-480-884A-152
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                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                  Patent No. 648259
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APPLICANT: Fan, Liqun
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PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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99.3%;
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Pred. No. 3e-268;
2; Mismatches
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TIVEL OF INVENTION: AND DIAGNOSIS OF LUNG CAN FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT TILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-542-615A-152
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US-09-542-615A-152
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99.3%;
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Pred. No. 3e-268;
2; Mismatches
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US-09-606-421B-152
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CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
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APPLICANT: L1, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya
APPLICANT: Hosken, Nancy
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TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 189
                                                                                                                                                   PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPSSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                               PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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99.3%;
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Pred. No. 3e-268;
2; Mismatches
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APPLICANT: Hosken, Nancy
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSTITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
TYPE: PRT
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GENERAL INFORMATION:
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APPLICANT:
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                                                                                       Kalos, Michael D.
Bangur, Chaitanya S.
Bosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                     PQGAVIRAMPYYKKAEHYTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYYEDP
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100.0%; Pred. No. 6.5e-242;
tive 0; Mismatches 0;
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APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FO

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA

FILE REFERENCE: 210121.455C8

CURRENT APPLICATION NUMBER: US/09/542,615A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SED ID NOS: 350

SOFTWARE: FastSEQ for Windows Version 3.0

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 344

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; GENERAL INFORMATION:
; APPLICANT: Wang, To
; APPLICANT: Fan, Liq
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Similarity 100.0%;
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Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S
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FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                     MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Search Job tim	В	Qy	Db	Qy	DЪ	Qy	DЬ
Search completed: August 7, 2003, 09:54:49 Job time : 19.8828 secs	481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511	481 SPTQALPPPLSMPSTSHCTPPPPPYPTDCSIV 511	421 GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL 480	421 GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTTIPDGMGANIPMMGTHMPMAGDMNGL 480	361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY 420	361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY 420	301 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360

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us-09-538-106-13.rapb

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 7, 2003, 09:46:34; Search time 27.3662 Seconds Run on:

(without alignments) 2781.719 Million cell updates/sec

US-09-538-106-13 3405 1 MSQSTQTNEFLSPEVFQHIW......FNFDMDARRNKQQRIKEEGE 641 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

451899 seqs, 118759770 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep: /cgn2_6/ptodata/1/pubpaa/US10_LRW_UB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			39, App	339, App	339, App	12, App	342, App	342, App	38, App	338, App	338, App	52, App	152, App	152, App	152, App	14, App	344, App
	Description	The section of the se	Sequence 33	Sequence	Sequence	Sequence 34	Sequence	Sequence	Sequence 33	Sequence	Sequence	Sequence 152, App	Sequence	Sequence	Sequence 1	Sequence 34	Sequence
	Ľ.		US-09-735-705-339	US-09-850-716A-339	US-09-897-778-339	US-09-735-705-342	US-09-850-716A-342	US-09-897-778-342	US-09-735-705-338	US-09-850-716A-338	US-09-897-778-338	US-09-735-705-152	US-09-850-716A-152	US-09-897-778-152	US-09-466-396A-152	US-09-735-705-344	US-09-850-716A-344
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Sequence 344, App Sequence 343, App Sequence 343, App Sequence 340, App Sequence 340, App Sequence 340, App Sequence 341, App Sequence 341, App Sequence 341, App Sequence 341, App Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 4, Appl Sequence 4, Appl Sequence 5, Appl Sequence 6, Appl Sequence 7, Appl Sequence 6, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 6, Appl Sequence 7, Appl Sequence 7, Appl Sequence 6, A	Sequence 3, Appli Sequence 4, Appli Sequence 36, Appl Sequence 28, Appl
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ALIGNMENTS

RESULT 1

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APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Eager, Neil
TTILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DISGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
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Pred. No. 4.5e-273;
); Mismatches 1;
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Sequence 339, Application US/09735705 Patent No. US20020052329A1
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aljun
Skeiky, Yasir A.W.
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; ORGANISM: Homo sapiens
US-09-735-705-339
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                                    GENERAL INFORMATION:
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APPLICANT: Kalos, Michael D.
APPLICANT: Raceally. Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE REFERENCE: 210121.455615
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
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Pred. No. 4.5e-273;
0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/897,778
NUMBER OF SEQ ID NOS: 467
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Pred. No. 4.5e-273;
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APPLICANT: Marnerakis, Margarita
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SEQ ID NO 339
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APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

TITLE OF INVENTION: COMPOSITIONS AND METHOMATICAL ASCIA

FILE REFERENCE: 210121, 455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FASTSEQ for Wind

SEQ ID NO 342

LENGTH: 600
                                               ; ORGANISM: Homo US-09-735-705-342
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; ORGANISM: HOMO US-09-850-716A-342
       Query Match
Best Local Sin
Matches 640;
                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 342, Application US/09850716A
Patent No. US20020115139A1
                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C15
                                                                                                                                                                                                                                                                                                          APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
                                                                                                                     LENGTH: 68
TYPE: PRT
                         Similarity
       Conservative
                                                                                                 sapiens
                       99.8%;
Score 3397; DB 10;
Pred. No. 1.1e-272;
0; Mismatches 1;
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APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 342
LENCTH: 680
TYPE: PRT
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US-09-897-778-342
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                                 ; ORGANISM: Homo sapiens US-09-897-778-342
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APPLICANT: Marnes
APPLICANT: Fanges
APPLICANT: Vedvic
APPLICANT: Cartes
APPLICANT: Watana
APPLICANT: Watana
                                                                                                                                                                                                                                                                                 Sequence 342, Application US/09897778 Patent No. US20020147143A1 GENERAL INFORMATION:
Best Local Similarity
         Query Match
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Watanabe, Yoshihiro
Henderson, Robert A.
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                                                                                                                                                                                                                                                                          Tongtong
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99.8%;
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Score 3397;
Pred. No. 1
 7; DB 10;
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            Length 680;
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SOFTWARE:
SEQ ID NO 3
LENGTH: 5
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                                                                                                                                                                                                                                           GENERAL INFORMATION
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                                                                                                               APPLICANT:
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                               CURRENT APPLICATION NUMBER: US/09/735, CURRENT FILING DATE: 2000-12-12 NUMBER OF SEQ ID NOS: 419
                                                                  TITLE OF INVENTION: COMPOSITIONS AT TITLE OF INVENTION: AND DIAGNOSIS FILE REFERENCE: 210121.455C14
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                      FastSEQ for Windows Version
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Fan, Liqun
                                                                                                     Fanger, Neil
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Bangur, Chaitanya S.
                                                                                                               McNeill, Patricia D.
                                                                                                                                       Skeiky, Yasir A.W.
                                                                                                                                                    Wang,
                                                                                                                                                             Fanger, Gary R.
Li, Samuel X.
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                                                                              COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
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APPLICANT: Retter, MARC W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIACNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENCTH: 586
                                               ; TYPE: PRT
; ORGANISM: Homo
US-09-850-716A-338
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; ORGANISM: Hom
US-09-735-705-338
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                                                                                                                                                                                      Sequence 338, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: Retter, Marc W.
 Query Match
Best Local Similarity
Matches 569; Conserv
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            99.5%;
 Score 3016; DB 10;
Pred. No. 3.1e-241;
1; Mismatches 2;
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Pred. No. 3.1e-241;
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          Query Match
Best Local Similarity
Matches 569; Conserv
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CURRENT APPLICATION NUMBER: US/09/897,778.
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-338
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-09-897-778-338
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 338, Application US/09897778 Patent No. US20020147143A1
                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                       APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIACROSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
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Conservative

99.5%;

Score 3016; DB 10; Pred. No. 3.1e-241; 1; Mismatches . 2;

Length

586; 0;

Gaps

0;

Gaps

134

74

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; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: HOMO s
US-09-735-705-152
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TITLE OF INVENTION: COMPOSITIONS AND METHO)
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG (
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTMARE: FastSEQ for Windows Version 3.0
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APPLICANT:
APPLICANT:
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    Best Local Similarity
                       Query Match
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Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Henderson, Robert A.
McNeill, Patricia D.
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Skeiky, Yas:
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Fan, Liqun
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      88.4%;
99.3%;
    Score
Pred.
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No. 1.2e-240;
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APPLICANT: MONEILL, PATTICIA D.
APPLICANT: MCNEILL, PATTICIA D.
APPLICANT: RETTER, MAIC M.
APPLICANT: RETTER, MAIC M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
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US-09-850-716A-152
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                                                              PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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  TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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pred. No. 1.2e-240;
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APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 152
LENGTH: 586
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                                              PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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Henderson, Robert A.
Peckham, David W.
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Vedvick, Thomas S.
Carter, Darrick
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Marnerakis, Margarita
                                                                               Conservative
                                                                                         88.4%;
99.3%;
                                                                             Score 3009; D:
Pred. No. 1.2e
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1.2e-240;
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US-09-466-396A-152
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SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 152
LENGTH: 586
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APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: DIAGNOSIS
FILE REFERENCE: 210121.455C4
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 152, Application US/09466396A Publication No. US20030119763A1
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99.3%;
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Pred. No. 1.2e-240;
2; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.6
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE DEFENDANCE: 10121 / 15521
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                                                                                                                                       SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180
                                                                                    DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                          PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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Fanger,
Li, Samu
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Skeiky, Yasir A.W.
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Best Local S
Matches 511
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CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
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ORGANISM: Homo
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                                                                   ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
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Search completed: August 7, 2003, 09:57:05 Job time : 28.3662 secs	481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511	481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511	421 GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL 480	421 GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL 480	361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY 420	361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLLQXQTSIQSPSSY 420
			IPDGMGANIPMMGTHMPMAGDMNGL 480	IPDGMGANIPMMGTHMPMAGDMNGL 480	YRQQQQQHQHLLQKQTSIQSPSSY 420	YRQQQQQHQHLLQKQTSIQSPSSY 420

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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MSQSTQTNEFLSPEVFQHIW.....FNFDMDARRNKQQRIKEEGE
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JH0631
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JH0631
R;de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A;Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A;Reference number: JH0631; MUID:92210006; PMID:1339362
A;Accession: JH0631
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A;Mccess
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A;Experimental source: liver
C;Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive
C;Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive
C;Superfamily: cellular tumor antigen p53
C;Reywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phc
E;164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
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45	44	43	42	41	40	39	38	37	36	ω 5	34	ω W	32	31	30
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149477	T34434	138972	A44068	S45251	JC7619	T13412	JH0797	T47149	A48666	в48666	T24089	G59436	T04518	H85335	JQ0110
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ALIGNMENTS

Оу	Db	Qy	Db	Qy	Db	Qy	Дb	· Qγ	Db	Qy	дъ	Qy	
361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 399 : : : : : : :	TKTKPAQGIKRAMKEASLPAP	309 PGRDRKADEDSIRKQQVSDSTKNGDGTKRPERQ-NTHGIQMTSIKKRRSPDDE 360	207 VPYEPPQVGSECTTVLYNFMCNSSCMGGMNRRPILTITLETQEGQLLGRRSFEVRVCAC 266	249 VPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICAC 308	148 LAIYKKLSDVADVVRRCPHHQSTSENNEGP-APRGHLVRVEGNQRSEYMEDGNTLRHSVL 206	189 MPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVL 248	CTYSPDLNKLFCQLAKTCPVQIV	129 NTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRA 188	40 GYDNEMMEAPLQVEFDPSLFEVSATEPAPQPSISTLDTGSPPTSTVPT 87	71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSPYAQPS-STEDALS-PSPAIPS 128	12 LSQESFEDLWSWV 39	11 LSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP 70	Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;

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cellular tumor antigen p53 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Nenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A29376; S61531; S72313; I51639
R;Soussi, T.; de Fromentel, C.C.; Mechall, M.; May, P.; Kress, M.
Oncogene 1, 71-78, 1987
A;Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a A;Reference number: A29376; MUID:88143684; PMID:2830576
A;Molecule type: mRNA
A;Residues: 1-363 <SOU>
A;Accession: A29376; MUID:88143684; PMID:2830576
A;Molecule type: mRNA
A;Cross references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; PID:g64962
R;Hoever, M.; Clement, J. H.; Wedlich, D.; Montenarh, M.; Knoechel, W.
Oncogene 9, 109-120, 1994
A;Title: Overexpression of wild-type p53 interferes with normal development in XA; Reference number: I51639; MUID:94134403; PMID:8302570
A;Accession: S61531
A;Molecule type: mRNA
A;Residues: 1-293,295-363 <HOE>
A;Cross references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514.
R;Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, W.
A;Accession: S72313
A;Accession: S72313
A;Accession: S72313
A;Accession: EMBL:X77546; NID:g468513: PIDN:CAA54672.1: PID:g468514.
A;Cross references: EMBL
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C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; F;150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-51,'s',53-70,72-293,295-363 <HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DALSPSPAIPSNTDYPGPHSEDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVM 177
                                                                                                                                            R---SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI
                                                                                                                                                                                                                                                         RRCFEARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKR 354
                                                                                                            LVVVDDDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV
                                                                                                                                                                                                                            RRCFEVRVCACPGRDRRTEEDNYTKKRGLKPSGK---
                                                                                                                                                                                                                                                                                                                                        EDVNSGRHSVCVPYEGPQVGTECTTVLYNYMCNSSCMGGMNRRPILTIITLETPQGLLLG
                                                                                                                                                                                                                                                                                                                                                                   EDPIIGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPPPRGSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SCAVPSTDDYAGKYGLQLDFQQNGTAKSVTCTYSPELNKLFCQLAKTCPLLVRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSETGMDPPLSQETFEDLWSLLPDPLQTVTCRLDNLS-EFPDYP------LAADMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQSTQTNEFLSPEVFQHIWDFLEQPI----CSVQPIDLNFVDEPSEDGATNKIEISMDCI
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42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GLMGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 777.5; DB 1
Pred. No. 3.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <HOW>
513; PIDN:CAA54672.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81;
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SS1048
SS1048
SS1048
R;Alternate names: tumor-suppressor protein p53
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #t
C;Accession: S51648
R;Dequiedt, F; Willems, L.; Burny, A.; Kettmann, R.
submitted to the EMBL Data Library, September 1994
a.nescription: Nucleotide sequence of the ovine p53
                               A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-386 <DEQ>.
A;Rosidues: 1-386 <DEQ
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A;Rosidues: 1-386 <DEQ>.
A;Rosidues: 1-386 <DEQ
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A;Rosidu
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S51648
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Nucleic Acids Res. 16, 11383, 1988
A;Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear once A;Reference number: S02193; MUID:89083584; PMID:3060861
A;Accession: S02193
A;Molecule type: mRNA
A;Residues: 1-367 <S0U>
A;Cross-references: EMBL:X13057; NID:963740; PIDN:CAA31456.1; PID:963741
A;Cross-references: EMBL:X13057; NID:963740; PIDN:CAA31456.1; PID:963741
C;Superfamily; cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleicular type site: zinc (Cys, His, Cys, Cys) #status predicted F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                               A; Accession: S51648
                                                                                                                                                                                                                                                                                                                                                   A; Reference number:
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C;Speciles: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: $02193
R;Soussi, T; Begue, A.; Kress, M.; Stehelin, D.; May, P.
   F;385/Binding
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   site: phosphoryl-RNA (Ser) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRETYEMLLKIKESLELMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRDRKIEEENFRK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYEPPEVGSDCTTVLYNFMCNSSCMGGMNRRPILTILTLEGPGGQLLGRRCFEVRVCACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDYGGDFDFRVGFVEAGTAKSVTCTYSPVLNKVYCRLAKPCPVQVRVGVAPPPGSSLRAV
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Pred. No. 2.9e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGGAGGVAKRAMSPPTEAPEPPK-KRYLNPDNEIFYLQVR
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Length

C; Date: 10. Sep-199 #sequence_revision 10. Sep-1999 #text_change 10. Sep-1999 C; Accession: S02192; S41149 R; SOUSSI, T; de Fromentel, C.C.; Breugnot, C.; May, E. Nucleic Acids Res. 16, 1134, 1988 A; Title: Nucleocide sequence of a cDNA encoding the rat p53 nuclear oncoprotein. A; Reference number: S02192; MUID:89083585; PMID:3060862 A; Accession: S02192; MUID:89083585; PMID:3060862 A; Accession: S02192 A; Molecule type: mRNA A; Residues: 1-391 *SOUD A; Cross references: EMBL:X13058; NID:956828; PIDN:CAA31457.1; PID:956829 R; Hulla, J.E.; Schneider, R.P. Nucleic Acids Res. 21, 713-717, 1993 A; Title: Structure of the rat p53 tumor suppressor gene. A; Reference number: S41149; MUID:93181268; PMID:8441680 A; Accession: S41149 A; Cross references: EMBL:X13059; NUID:93181268; PMID:8441680 A; Accession: S41149; MUID:93181268; PMID:8441680 A; Accession: S41449; MUID:93181268; PMID:8441680 A; Accession: S41449; MUID:93181268; PMID:8441680 A; Accession: S41149; MUID:93181268; PMID:8441680		Best Local s Matches 153 68 160 123 220 182 280
the one role of the order of th	Qy 419 SYGNSSPPLKMNSMKKLPSVSQL 442 : : ::: 1 : ::: 360 SRAHSSYPKTKKGQSTSRHKKPMIKKV 386 RESULT 6 JH0633 cellular tumor antigen p53 - golden hamster N.Alternate names: tumor-suppressor protein p53 C;Species: Mesocricetus auratus (golden hamster) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: JH0633 R;Legros, Y; MCIntyre, P; Soussi, T. Gene 112. 247-250. 1992	Db 92 SSSVPSQKTYQGNYGFHLGFLQSGTAKSVMCTYSISLNKLECQLAKTCPVQLMVTSTP 149 Qy 181 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEGNSHAQYVED 239

L.V.

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MOI. Cell. Biol. 6, 1379-1385, 1986
A;Title: Characterization of the human p53 gene.
A;Title: Characterization of the human p53 gene.
A;Reference number: A25224; MUID:87064416; PMID:2946935
A;Accession: A25224
A;Molecule type: DNA
A;Residues: 1-393 <LAM>
A;Residues: 1-393 <LAM>
A;Cess-references: EMBL:XO1405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1; PID
R;Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
Gene 70, 245-252, 1988
A;Title: A variation in the structure of the protein-coding region of the human p53 gene
A;Reference number: JT0436; MUID:89108008; PMID:2905688
A;Reference number: JT0436; MUID:89108008; PMID:2905688
A;Accession: A43073
A;Molecule type: DNA
A;Residues: 1-393 <BUC1>
A;Accession: JT0436
A;Accessio
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A; Residues: 101-393 < MKII>
A; Residues: 101-393 < MKII>
A; Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1; PID:g64224
R; Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M.
R; Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M.
EMBO J. 4, 1251-1255, 1985
A; Title: Human p53 cellular tumor antigen: cDNA sequence and expression
A; Reference number: A22837; MUID:85230577; PMID:4006916
A; Accession: A22837
A; Molecule type: mRNA
A; Residues: 1-71, 'P', 73-993 < ZAK>
A; Residues: 1-71, 'P', 73-993 < ZAK>
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A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 1-71, 'p', 73-272, 'H', 274-393 <HAR>
A;Residues: 1-71, 'p', 73-272, 'N', 274-393 <HAR>
A;Cross-references: GB:K03199; NID:g189478; PIDN:AAA59989.1; PID:g189479
A;Experimental source: clone pR4-2, cell line A431
R;Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.;
MO1. Cell. Biol. 6, 4650-4656, 103-2000; Prokocimer, M.; Wolf, D.; Arai, N.;
A;Title: Molecular basis for heterogeneity of the human p53 protein.
A;Reference number: A93086; MUID:87089826; PMID:3025664
                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; R;Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E. M01. Cell. Biol. 5, 1601-1610, 1985
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A;Title: Molecular cloning and in vitro expression of a cDNA clone for huma A;Reference number: A55060; MUID:85267676; PMID:3894933
A;Accession: A55060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Lamb, P.; Crawford, L. Mol. Cell. Biol. 6, 1379-1385, 1986
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A; Residues: 1-78, 'T', 80-393 <HAR1>
A; Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A; Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
A; Accession: B25397
                                                                                                                                                                  A;Status: LINE MRNA
A;Molecule type: mRNA
A;Residues: 1-247,'Q',249-393 <F08>
A;Residues: 1-247,'Q',249-393 <F08>
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A; Molecule type: mRNA
A; Residues: 1-247, 'Q', 249-393 <F06>
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A;Molecule type: mRNA
A;Residues: 1-192,'R',194-393 <F02>
A;Cross-references: EMBL:X60011; NID:g506434;
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A; Residues: 1-189, 'LLSILSEWKEICVWSIWMTETLFDIVWWCPMSRLRLALT', 'VPPSTTTTCVTVPAWAA'
A; Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
A; Note: deletion of a C nucleotide causes a frameshift at position 566
A; Accession: 138083
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R;Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.
EMBO J. 10, 2879-2887, 1991
A;Title: p53 is frequently mutated in Burkitt's lymphoma
A;Reference number: I38082; MUID:92007731; PMID:1915267
A;Accession: 138082
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A; Molecule type: mRNA; DNA
A; Residues: 66-79 < MKI3>
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A;Residues: 66-71,'P',73-79 <MKI2>
A;Experimental source: clone lambda
A;Note: 72-Cys was also found, and
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A; Residues: 1-71, 'P',
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A; Residues: 1-236, 'I', 238-393 <F05>
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A; Residues: 1-245, 'T', 247-393 <F04>
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A;Accession: I38085
                                       A; Molecule type: mRNA
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A; Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
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A;Status: translated from GB/EMBL/DDBJ
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   ',73-162,'H',164-393 <F09>
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EMBL:X60015; NID:g506442;
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PMID:3547088
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           PIDN:CAA42633.1;
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                                                                                                                                                                                              PID: 9506447
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<F01>

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A;Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1; PID:g232816
R;Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1933
A;Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lyn
A;Reference number: I52681; MUID:94036762; PMID:8221626
A;Accession: I52681
A;Status: translated from GB/EMBL/DDBJ
A;Cross-references: GB:S6666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A;Cross-references: GB:S6666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A;Cross-references: GB:S66666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A;Cross-references: GB:S6666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A;Cross-references: GB:S6666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A;Cross-references: GB:S6666; NID:g436293
A;Cross-references: GB:S66666; NID:g436292; PIDN:AAB28601.1; PID:g436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: p53 gene mutations in gastric cancer metastases and in gastric cance A;Title: p53 gene mutations in gastric cancer metastases and in gastric cance A;Reference number: A44905; MUID:92034678; PMID:1933850
A;Recession: A44905
A;Accession: A44905
A;Accession: A469247, 'W',249-250 <YAM>
A;Residues: 246-247, 'W',249-250 <YAM>
A;Residues: 246-247, 'W',249-250 <YAM>
A;Residues: 246-247, 'W',249-250 <YAM>
A;Cross-references: GB:S63157; NID:9237829; PIDN:AAB20140.1; PID:9237830
A;Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBIP:63158)
A;Note: mutation from a liver metastasis of a gastric cancer R;Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
Oncogene 5, 1067-1071, 1991
A;Title: Use of the single strand conformation polymorphism technique and PCI A;Reference number: I58354; MUID:9129386; PMID:1648702
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 244-247, 'W',249-252 <HENI>
A;Cross-references: GB:S41969; NID:91679931; PIDN:AAB19324.1; PID:9232814
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A:Status: preliminary; translated from A:Molecule type: DNA
A:Residues: 274-277,'S',279-282 <HEN2>
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A; Status: translated from GB/1
A; Molecule type: mRNA
A; Residues: 1-212,'Q',214-393
A; Cross:references: EMBL:X600
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A; Residues: 1-393 <FUT>
A; Cross-references: EMB
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A; Status: translate
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1, 5800-5805, 1991
                                                                           LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP 70
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la, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi,
                                                                                                                                                                                                            21.1%; 38.4%;
                                                                                                                                                                Score 718; DB 1;
Pred. No. 5.2e-42;
69; Mismatches 132;
-NNVLSPLPSQAMDDLMLSPDDIEQWFTE--DP---
                                                                                                                                                                                                                                                Length 393
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A; Molecule type: mRNA
A; Residues: I-159, 'H',161-167, 'G',169-233, 'I',235-390 <ZAK>
A; Residues: I-159, 'H',161-167, 'G',169-233, 'I',235-390 <ZAK>
A; Cross-references: GB:X01237; GB:K01700; NID:g53575
R; Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Sh
Woll Cell. Biol. 6, 3232-329, 1986
A; Title: Immunologically distinct p53 molecules generated b;
A; Reference number: S38822; MUID:87064640; PMID:3023970
A; Accession: S38822
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EMBO J. 3, 2179-2183, 1984
A;Title: Analysis of the gene coding for the murine cellular
A;Reference number: A22739; MUID:85027173; PMID:6092064
A;Accession: A22739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellular tumor antigen p53 - mouse
N;Alternate names: oncoprotein p53
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C;Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioorg. Khim. 13, 1691-1694, 1987
A; Title: Primary structure of DNA complementary to murine A; Reference number: S06336; MUID:88221682; PMID:3329909
A; Accession: S06336
                                                                                                                                                                                                                                                                                                                                                                     Nature 306, 594-597, 1983
A;Title: A single gene and a pseudogene for the cellular A;Reference number: A02684; MUID:84068204; PMID:6646235
A;Accession: A02684
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A; Residues: 1-390 < ARA1>
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A; Residues: 1-13
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                     A; Cross-references:
                                                A; Residues:
                                                                 A; Molecule type:
                                                                                              A; Accession: S38823
                                                                                                                  A;Cross-references:
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A; Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1;
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                                           ype: mRNA
1-167,'G',169-233,'I',235-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-134,'V',136-390 <CHU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum,
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EMBL:M13873
D.; Yokota, K.;
                                                                                                                  EMBL:M13872;
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                                                                                                               NID:g200198;
                                                <ARA2>
                                                                                                                  PIDN: AAA39881.1;
                                                                                                                                                                                                                                                                              Shohat,
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                                                                                                               PID:g200199
                                                                                                                                                                                                                                                                                  O.; Rotter,
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Wolf, D.; Brill,

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Shohat,

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Rotter,

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submitted to the EMBL Data LIDILLA, A; Reference number: $40014
A; Accession: $40014
A; Molecule type: mRNA
A; Residues: 1-167, 'G', 169-390 <ARA3>
A; Residues: 1-167, 'G', 169-390 <ARA3>
A; Coss-references: EMBL.M13873; NID: 9200200; PIDN: AAA39882.1;
A; Cross-references: AAA39882; AA
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A; Molecule type: mRNA
A; Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>
A; Cross-references: EMBL:X00741; NLD:g53570; PIDN:CAA25323.1; PID:g53571
C; Comment: This DNA-binding protein plays an essential role in the regula C; Comment: The tetramer association region may exhibit a beta-turn, beta-c; Superfamily: cellular tumor antigen p53
C; Keywords: apoptosis; cell division control; DNA binding; homotetramer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \begin{array}{lll} F; 313-319/\text{Region: nuclear location signal} \\ F; 319-357/\text{Region: tetramer association} \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;99-289/Domain: DNA-binding core #status predicted F;108-121/Region: L1 loop F;114-139/Region: conserved region II F:160-192/Region: L2 loop F;168-178/Region: conserved region IV F;231-252/Region: conserved region IV F;233-248/Region: L3 loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1-44/Domain: transcription activation \#status predicted F;16-26/Region: conserved region I
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A;Title: Cloning and expression analysis of full length A;Reference number: 148703; MUID:84272240; PMID:6379601
A;Accession: 148703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: translated from GB/EMBL/DDBJ
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Best Local
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371
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                                                                                                                                                                                                                                                       IKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIE--
                                                                                                                                                                                                                                                                                                                                                                          NSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDA
GQSTSRHKKTMVKKVGPDS
                                                   QQQQQQHQHLLQKQTSIQS
                                                                                                         POKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---AHATEESGDSRAHSSYLKTKK 370
                                                                                                                                                                                                                         SSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEVLCPELPPGSAKRALPTCT---SASP
                                                                                                                                                                                                                                                                                                                                         NLYPEYLEDRQTFRHSVVVPYEPPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHE---RCSDGDGLAPPQHLIRVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEG
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38.0%;
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Pred. No. 6e-42;
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A;Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphop A;Reference number: S06594; MUID:90045967; PMID:2530498
A;Recession: S06594
A;Molecule type: mRNA
A;Residues: 1-393 <RIG>
A;Cross references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetrammer; nuc F:176,179,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellular tumor antigen p53 - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S06594
R;Rigaudy, P.; Eckhart, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Rigaudy, P.; Eckhart, W. Nucleic Acids Res. 17, 8375,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                              VRGRETYEMLLKIKESLEL
                                                                                                                                                                                                                                                             RAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSP----SPAI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSQETFSDLWKLLPE-----NVLSPLPSQAVDDLMLSPD------DLA--QW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                             ACPGRDRRTEEENFRKKGEPCHELPPGSTKRALPNNT----SSSPQPKKKPLDGEYFTLQ
                                                                                                                                                                                                                                 VVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVC
                                                                                                                                                                                                                                                                                                                                                  RAMAIYKQSQHMTEVVRRCPHHE--RCSDSDGLAPPQHLIRVEGNLRVEYSDDRNTFRHS
IRGRERFEMFRELNEALEL
                                                                                                                                                                 ACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDELLYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSQKTYHGSYGFRLGFLHSGTAKSVTCTYSPDLNKMFCQLAKTCPVQLWVDSTPPPGSRV
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41.2%;
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A; Cross-references: GB:M13874; NID:9200202; PIDN:AAA39883. R; Han, K.A.; Kulesz-Martin, M.F. Nucleic Acids Res. 20, 1979-1981, 1992 A; Title: Alternatively spliced p53 RNA in transformed and A; Reference number: S35478; MUID:92253421; PMID:1579500 A; Accession: S35478 C;Accession: S38824; S35478
R;Aral, N.; Nomura, D.; Yokota, K.;
Mol. Cell. Biol. 6, 3232-3239, 1986
A;Title: Immunologically distinct p5 A;Status: nucleic acid sequence not shown; A;Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-381 < ARA> A; Reference number: S38822; A; Accession: S38824 cellular tumor antigen p53, minor splice form - mouse C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change stinct p53 molecules MUID:87064640; PMID: Wolf, . : translation pMID:3023970 PIDN: AAA39883.1; Brill, [F] : not shown Ьy normal cells of different PID:g200203 alternative splicing 23-Jul-1999 0.;

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A; Residues: 1-381 <hAN>
A; Cross-references: EMBL:M13874; NID:9200202; PIDN:AAA39883.1; PID:9200203
A; Otto: the nuclectide sequence was submitted to the EMBL Data Library, July 1988
C; Comment: This sequence, produced by alternative splicing of the tenth intron, lacks the not known.
C; Superfamily: cellular tumor antigen p53
C; Reyvords: alternative splicing; phosphoprotein; zinc
F; 1-44/Domain: transcription activation #status predicted <TRA>
F; 16-26/Region: conserved region I
F; 99-289/Domain: DNA-binding core #status predicted <DBC>
F; 108-121/Region: L1 loop
F; 108-121/Region: conserved region II
F; 160-192/Region: conserved region IV
F; 231-252/Region: conserved region IV
F; 231-252/Region: conserved region IV
F; 333-48/Region: conserved region V
F; 313-319/Region: nuclear location signal
F; 319-357/Region: nuclear location signal
F; 319-357/Region: tetramer association
F; 7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F; 312/Binding site: phosphate (Ser) (covalent) #status predicted
F; 312/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                      tumor suppressor protein p53 - Chinese hamster C;Species: Cricetulus griseus (Chinese hamster) C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 C;Accession: JC6176 R;Lee, H.; Larner, J.M.; Hamlin, J.L.
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A; Reference number: JC6176;
A; Contents: liver
A; Accession: JC6176
A; Molecule type: mRNA
                                                           R;Lee, H.; Larner, J.M.; Hamlin, J.L.
Gene 184, 177-183, 1997
A;Title: Cloning and characterization of Chinese hamster
A;Reference number: JC6176; MUID:97183659; PMID:9031625
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;319-357/Region: tetramer association
;319-357/Region: tetramer association
;719-12.18.23.37/Bhinding site: phosphate (Ser) (covalent) #status predicted
;173.176.235,239/Binding site: zinc (Cys. His. Cys. Cys) #status predicted
;173.176.235,239/Binding site: covalent) (by cdc2 kinase) #status predicted
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A; Gene: p53
C; Superfamil
C; Keywords:
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R;Le Goas, F.; May, P.; Ronco, P.; de Fromentel, C.C.
Gene 185, 169-173, 1997
A;Title: cDNA cloning and immunological characterization
A;Reference number: JC6193; MUID:97208869; PMID:9055811
A;Accession: JC6193
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                                                                                                                                                                                        A:Gene: p53
C:Superfamily: cellular tumor antigen
C:Keywords: tumor
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A; Residues: 1-391 <LEA>
                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997
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157; Conserv
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                            QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL-SPSPA----
                                                                                             LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
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----VANWLNEDPEEGLRVPA---
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  p53 - rabbit
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                                                                                                                                         20.5%;
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41.6%; Pred. No. 5.2e-41;
                                                               -PENNLLTTSLN--
                                                                                                                          59;
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                                                                                                                         Score 699.5;
Pred. No. 9.7e
59; Mismatches
                                                                                                                                                                                                                                                       NID:g1532043; PIDN:CAA62216.1; PID:g1532044
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1; Mismatches
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                                                                                                                          5; DB 2;
9.7e-41;
hes 111;
- APAPEA - PAPAAPALAAPAPATSWP
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                                                                                                                                                        Length 391;
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                                                               DLLSAED
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RESULT 14
T19361
hypothetical protein C17G1.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.
C;Accession: T19361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
146226
cellular tumor antigen p53 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-196226
C;Accession: 146226
  A; Map position: 1
A; Introns: 40/3;
                           A; Genetics:
                                       A; Experimental source:
C; Genetics:
                                                             A; Cross-references: EMBL: 278415;
                                                                                                              A; Reference number: A; Accession: T19361
                                                                                                                          submitted to the EMBL Data A; Reference number: Z19114
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                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns:
C; Superfam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Anticancer Res. 14, 2039-2046, 1994
A;Title: The canine p53 gene is subject to somatic mutations in A;Reference number: I46226; MUID:95150524; PMID:7847847
A;Accession: I46226
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                                                                                      A; Molecule type: DNA
                                                                                                 A; Status: preliminary; translated
                                                                                                                                                   R; White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues:
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A; Residues: 1-77 <DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                ;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                 Matches
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                           CESP:C17G1.4
                                                                                                                                                                                                                                                                                   254 POVGTEFTTVLYNEMCNS
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                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                            KAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF
                                                                                                                                                                                                                                                              PEVGFDYTTIHYNYMCNS
                                                                                                                                                                                                                                                                                                              KSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAKYLDDRYTFRHSVVVPYEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVRVCACPGRDRRTEEENFRKKGEPCPELPPGSSKRALPTTT--TDSSPQTKKKPLDGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFRHSVVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTITLEDSSGNLLGRNSF
                                                                                                                                                                                                                                                                                                                                                                                                                cellular
                                                                                                                                                                                                                                                                                                                                                                                                                            61/3
   98/2;
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <DEV>
                                                                                                                                                                        #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:L27630;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translated from GB/EMBL/DDBJ
 295/1; 443/3;
                                                    clone
                                                                                                                                                                                                                                                                                                                                                                                                              tumor antigen
                                                                                                                                                                                                                                                                                                                                                                        7.6%;
                                                                                                                                     Library, August
                                                   C17G1
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                                                                                                                                                                                                                                                                77
                                                               PIDN:CAB01670.1;
                                                                                                                                                                                                                                                                                                                                                            Score 259.5; DB 2;
Pred. No. 2.2e-11;
6; Mismatches 14;
                                                                                                   from GB/EMBL/DDBJ
590/3; 619/3; 691/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN: AAC37327.1;
                                                               GSPDB:GN00028;
                                                                                                                                                                                                                                                                                                                                                                                   Length
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810/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID: g508455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thypoid carcinoma
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                        Matches
                                      Best
                                                Query Match
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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1621 <JOH>
A; Cross-references: EMBL:AF003386; NID:g2088833; PID:g2088843; PIDN:AAB54259.
                                                                                                                                                                                                                                                                                                                                  RiJohnson, D.
RiJohnson, D.
Submitted to the EMBL Data Library, May 15
                                                                                                                                                                                                                                                                                                  A; Description: The sequence
A; Reference number: Z18318
A; Accession: T15264
                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F59E12.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #te:
                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated
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Matches 127; Conservative
                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FNEGQIAPPSHLIRVEG-NSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSPMGSSLMPLNGQYPSMTQNMQSPASTSMEPTFKEPAVPIRHSPSQMPTHLQSPVHPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGAPPA-YNAPSSSKT-PDPTQQQRPHS--PTFAVPTLPAAATLAQAFSANQISTK-PKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPQHTIETYRQQQQQQHQHLLQKQTSI---QSPSSYGN-----SSPPLNKMNSMNKL
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                                                                                                                        55/1;
                                          Conservative
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                                                                                                                   200/2; 299/2; 327/2; 369/3; 589/3; 860/1; 986/1; 1278/1; 1547/
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  -FLSPEVFQHIWDFLEQPICSVQPIDL---
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                                                                                                                                                                                                                                                                                    from
                                                           Score 144.5; D
Pred. No. 0.14;
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                                                                             DB 2;
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                                          239;
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Search completed: August 7, 2003, 09:53:19 Job time : 23.2089 secs THIS PAGE BLANK (USPTU)

Run on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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      SwissProt_41:*
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    P73_HUMAN
P73_CERAE
P53_ORCH
P53_BARBU
P53_ICTPU
P53_ICTPU
P53_FELCA
P53_PICA
P53_PICA
P53_PICA
P53_CAVIA
P53_CAVIA
P53_CAVPO
P53_RAT
P53_CAVPO
P53_HUMAN
P53_MACFA
P53_MACFA
P53_MACFA
P53_CAVPH
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P53_CAICMA
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6 mesocricetu
6 platichthys
7 homo sapien
0 mus musculu
3 macaca fasc
1 cercopithec
4 macaca mula
8 xiphophorus
3 xiphophorus
5 cricetulus
6 oryctolagus
2 spermophilu
2 equus cabal
0 equus asinu
                                                                                                                                                                                                                                                                                                              8 bos taurus
6 marmota mon
1 rattus norv
6 cavia porce
1 tupaia glis
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Result No.

Score

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718 718 717 715.5 714.5 713.5 710.5 700.5 707.5 699.5 699.5 689.5

Minimum DB : Maximum DB :

Searched:

Scoring table: Sequence: Title: Perfect score:

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V70K_TYMV	T2D3_DROME	TLE4_HUMAN	YQKA_SCHPO	SPY_DROME	TLE4_MOUSE	V70K_TYMVC	TUSP_HUMAN	ZAP3_MOUSE	ABL_DROME	GALY_YEAST	PCLO_HUMAN
P10357 turnip yell									P00522 drosophila		Q9y6v0 homo sapien

ALIGNMENTS

RTRARRRR	RRRRRRRR	R R R R R R R R R R R R R R R R R R R	RR RA RR R	R R R R R R R R R R R R R R R R R R R	P73_HU P73_HU P73_HU ID P AC O AC O DT 1 DT 1 DT 1 DT 1 OC DE T OC O OC H OC N OC N
SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA). TISSUE-Breast cancer, Hepatoma, Lymphocytes, and Skin; MEDLINE-99310938; PubMed-10381648; De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G., Costanzo A., Levrero M., Knight R.A.; "Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splicing variants epsilon and zeta.";	MEDLINE-99021697; PubMed-9802988; De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M., Annicchiarico-Petruzzelli M., Levrero M., Melino G.; "Two new p73 splice variants, gamma and delta, with different transcriptional activity."; J. Exp. Med. 188:1/63-1/68(1998).	SEQUENCE FROM N.A. (ISOFORM ALPHA). MEDLINE-98389621; PubMed-9721206; Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., Jenkins R., Smith D.I., Liu W.; "Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions."; Genomics 51:359-363(1998). [4] SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA). TISSUE-Neuroblastoma:	[2] SEQUENCE FROM N.A. (ISOFORM ALPHA). SEQUENCE FROM N.A. (ISOFORM ALPHA). MEDLINE-99289209; PubMed-10362363; YOShikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K., Harris C.C.; "Mutational analysis of p73 and p53 in human cancer cell lines."; Oncogene 18:3415-3421(1999). [3]	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA). SEQUENCE-Colon; MEDLINE-97433090; PubMed-9288759; MEDLINE-97433090; PubMed-9288759; Kaghad M., Bonnet H., Yang A., Creancier L., Biscan JC., Valent A., Minty A., Chalon P., Lelias JM., Dumont X., Ferrara P., McKeon F., Caput D.; "Monoallelically expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers."; Cell 90:809-819(1997).	HUMAN P73_HUMAN STANDARD; PRT; 636 AA. 015350; 015351; Q9NTK8; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Tumor protein p73 (p53-like transcription factor) (p53-related protein). TP73 OR P73. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99217940; PubMed=1020327
Kaelin W.G. Jr.;
"The emerging p53 gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION
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Kharbanda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to DNA damage.";
Nature 399:814-817(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99318135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99380160; PubMed=10449409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                 TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER, SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
INDUCTION: NOT INDUCED BY DNA DAMAGE.
DOMAIN: POSSESS AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.
DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. 18.4438-4445(1999).

FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE. WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
SIMILARITY:
                                                                                                                                                                                                                                                                                  Name-Zeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
                    NEUROBLASTOMA AND
                                                                                                                                                                                                                                                                                                                                                                                 Name=Epsilon;
                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Delta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT:
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Note=The splicing c
original reading fr
reading frame to th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H., banda S., Welchselbaum R., Kufe D.; is regulated by tyrosine kinase c-Abl in the apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Death
                                                                                                                                                                                                                                                           IsoId=015350-6;
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BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORMS ALPHA AND BETA).
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  IN DIVER.
OCCUPANTE TO P53. HEMIZYGOSITY IS OBSERVED IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN CLIGODENDROGLIOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence=VSP_006540, ng of exon 11 results
                                                                                                                                                                                                                      Sequence=VSP_006538;
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XAC977624; AAC61887.1;
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XAC977626; AAC61887.1;
XAC977627; AAC61887.1;
XAC977628; AAC61887.1;
XAC979084; AAD39696.1;
XAC979082; AAD39696.1;
XAC979084; AAD39696.1;
XAC99085; AAD39696.1;
XAC99086; AAD39696.1;
XAC99086; AAD39696.1;
XAC99088; AAD39696.1;
XAC99088; AAD39696.1;
XAC99091; AAD39696.1;
XAC99093; AAD39696.1;
XAC9093; AAD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601990;
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                                                                                                                                                                                                                                                                                                                                                                                                                            ion regulation; Activator; DNA-binding; Anti-oncogene;
Nuclear protein; Phosphorylation; Alternative splicin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       email to license@isb-sib.ch).
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isoform Kappa).

FTIG-VSP_006538.

SFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPE
SFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPE
QYRMTIWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGE
LQRQRYMEAVHFRVRHTITIPNRGGPGGGPDEWADFGFDLP
DCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
                                                                                                                                           BETA)
                                                                                                                                                                                                                                                                                      MEDIATES POLY-PRO.
                                                                                                                                                                                            PHOSPHORYLATION
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NUCLEAR LOCAL
                                                                                                                                                                                                                                                                                                                                                                                   TRANSACTIVATION
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LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                            OLIGOMERIZATION (POTENTIAL).
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Best Local 9
                                                                                                                                                                                                                                      _CERAE
                                                                                                                                               O9XSK8: Q9TSQ9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor protein p73 (p53-like transcription factor) (p53-related
                                                                            Cercopithecus aethiops (Green monkey) (Grivet).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                     Cercopithecinae;
                                                                                                                           TP73 OR P73.
                                                                                                                                                                                                                       P73_CERAE
               TISSUE-Kidney;
                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 366; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKEE 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQTSIQSPSSYGNSSPPLNKMN-SMNKLPSVSQLIN--PQQRNALTPTTIPDGMGANIPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVLGRRCFEARICACPGRDRKADEDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSQSTQTNEFLSPE----VFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKI----EIS
                                                                                                                                                                                                                                                                                                                                               AATISIGGSGELQRQRVMEAVHFRVRHTITIPNRGGPGGGPDEWADFGFDLPDCKARKQP
                                                                                                                                                                                                                                                                                                                                                                       ASTVSV-GSSETRGERVIDAVRFTLRQTISFPPR-----DEWNDFNFDMDARRNKQQR
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                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPPPYPTDCSIVSFLARLGCSSCL
                                                                     Cercopithecus.
                            (ISOFORMS ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SPDGGTTFEHLWSSLEP-----DSTYFDLPQSSRGNNEVVGGTDSS
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Pred. No. 2
                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                      637
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE DAN DAMAGE.
-- FUNCTION: PROMICED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00348; P53; 1.
Transcription regulation; Ac
Apoptosis; Nuclear protein;
VARSPLIC 495 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002117; P. InterPro; IPR001660; S. Pfam; PF00870; P53; 1. Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y11419; CAA72224.1;
EMBL; Y11419; CAA72225.1;
HSSP; O15350; 1COK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOId-Q9XSK8-2; Sequence-VSP_006537;
DOMAIN: POSSESS AN ACIDIC TRANSACTIVATION DOMAIN, A CE
BINDING DOMAIN AND A C-TERMINAL OLICOMERIZATION DOMAIN
TO THE ABL TYROSINE KINASE SH3 DOMAIN.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
SUBURIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms-2;
                                                                  163
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                                                                                                                                                                                                                                                                                                     Similarity
                         AQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDG
                                                                                IKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSH
                                                                                                                     MDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP
                                                                                                                                                                                                                                   MAQSTTT----SPDGGTTFEHLWSSLEP-----DSTYFDLPQSSRGNNEVVGGTDSS
                                                                                                                                                                                                                                                             MSQSTQTNEFLSPE----VFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKI----EIS
                                                                                                                                                                            MDVFHLEGMTTS-----VMAQFNLLSSTMDQMSSRAASASPYTPEHAA-SVPTHSPYAQP
                                                                                                                                                                                                                                                                                                                                                637
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                               69630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53.
                                                                                                                                                                                                                                                                                                   54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                 Activator; DNA-binding; Anti-oncogene;
n; Phosphorylation; Alternative splicing.
SFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPE
QYRMTIRMGLQDLKQGHDYGAAAQQLLRSSNAAAISIGGSG
ELQRQRVMEAVHFRVRHTITIPNRGGPGAGPDEWADFGFDL
                                                                                                                                                                                                                                                                                                                                               WW.
                                                                                                                                                                                                                                                                                         95;
                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                   Score 1769.5;
                                                                                                                                                                                                                                                                                                                                             /FTId=VSP_006537.
7CB200B919C9C70A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       PDCKARKQPIKEEFTEAEIH ->
                                                                                                                                                                                                                                                                                      ed. No. 6.2e-112;
Mismatches 150;
                                                                                                                                                                                                                                                                                                                  DB 1;
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Indels Length

Gaps

17

5

48

173

102

162

233 222

637; 59;

RTWGP (in

ISOIOTM

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PSSULP

PSSULP
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01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
7-11-1ar tumor antigen p53 (Tumor suppressor
                                                                                                                                                                                                                                                 This SWI
                                                                                                           use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92210006; PubMed=1339362; de Fromentel C.C., Padkel F., Chapus A., "Ratanbow trout p53: cDNA cloning and bioc Gene 112:241-245(1992).

-I- FUNCTION: Acts as a tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Neopterygii; Teleostei; Euteleostei;
                                                               EMBL; M75145; AAA49605.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
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                                                                                                                                                                                                                                                                                                                                                                                                      growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                         expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                      JH0631; JH0631
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SEQUENCE FROM N.A.

Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;

"Evolutionary conservancy of p53 gene sequences in fish.";

"Evolutionary conservancy of p53 gene sequences in fish.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.
                                                                                                                                                                                                                                                              Actinopterygii; Neopterygii; Cyprinidae; Barbus. NCBI_TaxID=40830;
                                                                                                                                                                                                                                                                                                                                                                              16-0CT-2001 (Rel. 40, Createq)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NA-binding; Transcription regulation; Phosphorylation; Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281
356
392
318
                                                                                                                                                                                                                                                                                                                                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43966 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 847.5; I
Pred. No. 4.8e-
61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tion; Apoptosis.
TRANSCRIPTION ACTIVATION
BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                            Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8422250765545A1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         847.5; DB 1;
No. 4.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369
                                                                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---KMNLNLVAVQPPETE----SWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                        _BRARE
P53_BRARE STANDARD; PRT; 373 AA.
P79734; Q90440;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor)
TP53 OR DRP53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Phosphorylation; Approximation of Transcription of 28 By SIM:
DALBIND 66 256 BY SIM:
DOMAIN 298 329 OLIGOMI
DOMAIN 342 365 BASIC DOMAIN 342 365 BASIC DOMAIN 276 292 NUCLEAR MOD_RES 368 368 PHOSPHOREM
Brachydanio rerio (Zebrafish) (Danio Eukaryota; Metazoa; Chordata; Craniat Actinopterygii; Neopterygii; Teleoste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF071570; AAD34212.1; -. HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ptam; PF00870; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptosis
BAX and F/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
                                                                                                                                                                                                                                                                                                                                                                                                      374
                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLYNFMCNSSCMGGMNRRPILTIISLETHDGQLLGRRSFEVRVCACPGRDRKTEESNFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLYNFMCNSSCYGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSF 142
                                                                                                                                                                                                                                                                                                                                                                                                    MLLKIKESLELMQYLPQHTIETYRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQ---ETKTLDKIPSANKRSLTKDSTSSVPRPEGSKKAKLSGSSDEEIYTLQVRGKERYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQVSDSTKNGD----GTKRPF-RQNTHGIQMTSIKKRR----SPDDELLYLPVRGRETYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQSGTAKSVTCTYSSDLNKLFCQLAKTCPVQMVVNVAPPQGSVIRATAIXKKSEHVAEVV
                                                                                                                                                                                                                                                                                                                                                     MLKKINDSLELSDVVPPSEMDRYRQK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELINDEYLPSSFDPNIFDNVLTEQPQPSTSP-----PTASVPVATDYPGEHGFKLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
66
298
342
376
368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is induction seems to be mediated either by stimulation FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41233 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.1%;
51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ig; Transcription regulation; Activator;
ylation; Apoptosis.
TRANSCRIPTION ACTIVATION (ACIDIC).
BY SIMILARITY.
OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
MW; OBEZCF2CEA74C304 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 819.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                               suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                    399
                       rerio).
ta; Vertebrata;
Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3e-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                         Euteleostomi;
Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195
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                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                   MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S., Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.; "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence expression during embryogenesis."; Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein; Phosphorylation; Apoptosis.

DOMAIN 1 31 TRANSCRIPTION ACTIVATION
DNA_BIND 70 260 BY SIMILARITY.

DOMAIN 301 332 OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U60804; AAB40617.1; -
EMBL; U46693; AAA97408.1; -
HSSP; P04637; 1TUP.
ZFIN; ZDB-GENE-990415-270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002117; Pfam; PF00870; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Winge P.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 140-212 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97344388; PubMed=9200835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BCl-2 expression (By similarity). SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                             169
                                                                                                                        292
                                                                                                                                                                                                                                                      158;
                                                                                                                                                                                                                     112 QPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
                                                                                                                                                                                                                                                                   Similarity
                DGQVLGRRCFEARICACPGRDRKADEDSIRK-QQVSDSTKNGDGTKRPFRQNTHGIQM---
                                                           QPST----LPPTSTVPETSDYPGDHGFRLRFPQSGTAKSVTCTYSPDLNKLFCQLAKTCP
EGQLLGRRSFEVRVCACPGRDRKTEESNFKKDQETKTMAKTTTGTKRSLVKESSSATLRP
                                                                                            SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR
                                                                                                                                                                                                                                                                                                                  70
301
345
345
280
372
373 AA;
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                    260
332
366
296
372
                                                                                                                                                                                                                                                                                                                     41899 MW;
                                                                                                                                                                                                                                                                     23.7%;
53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .
                                                                                                                                                                                                                                                      42; Mismatches
                                                                                                                                                                                                                                                                     Score 805.5; DE Pred. No. 3e-47;
                                                                                                                                                                                                                                                                                                                                  NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                BASIC (REPRESSION OF
                                                                                                                                                                                                                                                                                                                     AC7AB724FA6B61FF CRC64;
                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                      82;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                DNA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                                                              (ACIDIC)
                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                           228
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                                                                                                                 Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                DNA_BIND
DOMAIN
DOMAIN
                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P53_ICTPU STANDARD; PRT; 376 AA. 093379; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor PF53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF074967; AAC26824.1; HSSP; P04637; ITUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luft J.C., Bengten E., Clem L.W., Miller N.W., "Identification and characterization of the tunchannel catfish (Ictalurus punctatus)."

Comp. Biochem. Physiol. 120B:675-682(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ictalurus punctatus (Channel Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00348; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=99071979; PubMed=9854815;
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7998
                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                            108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P04637;
        56
                                                                                                                                             Similarity
                                                       SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA
        SDMLQPQSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGSKKAKGSSSDEEIFTLQVRGRERYEILKKLNDSLELSDVVPASDAEKYRQK 341
                                                                                                                   Conservative
                                                                                                                                                                                                                                  A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation; Apoptosis.
36 TRANSCRIPTION ACTIVATION
- SSPTTSTVEVTSDYPGLLNFTLHFQESSGTKSVTCTYSPDLNKLFCQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Channel catfish).
Chordata; Craniata;
                                                                                                                                                                                                                                  41989
                                                                                                                                             23.3%;
                                                                                                                                                                                                                                  M
                                                                                                                   44;
                                                                                                              Score 795; DB
Pred. No. 1.5e
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Teleostei;
                                                                                                                                                                                                                            BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
1B89CD98DB3289F2 CRC64;
                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the tumor
                                                                                                                                           DB 1;
.5e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson
                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  suppressor p53
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.R.;
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D53_XENLA
ID P53_X
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D77 01-Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REDIENCE FROM N.A.

REDIEN
                           EMBL; M36962;
EMBL; X05191;
EMBL; X77546;
EMBL; S68353;
EMBL; S68353;
PIR; A29376; A
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P07193;
01-APR-1988
                                                                                                                                                                                                                                         or send
                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinfo
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soussi T., de Fromentel C.C., Mechali M., May P., Kress M.; "Cloning and characterization of a cDNA from Xenopus laevis for a protein homologous to human and murine p53."; Oncogene 1:71-78(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; (
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1988
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-88143684; PubMed-2830576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae;
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                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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KTCPVLMAVSSSPPPGSVLRATAVYKRSEHVAEVVRRCPHHERSNDSSDGP-APPGHLLR
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                                                              ; AAA49923.1;
; CAA28821.1;
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                                                                                                                                                                                                                                  license agreement (See http://www.isb-sib.ch/announce/license@isb-sib.ch).
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Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clawed frog)
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InterPro; IPR002117; P53.

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DOMAIN
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DOMAIN
                                                                                                                                                                      P53_TETMU STANDARD; PRT; 367 AA.
Q9W679;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor)
TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
"Evolutionary conservancy of p53 gene sequences in fish.";
Submitted (JUN1-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Acts as a tumor suppressor in many tumor type
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.
                                                   TISSUE=Ovary;
                                                                                          NCBI_TaxID=94908;
                                                                                                                                                          Tetraodon miurus (Congo puffer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                            242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 VLQE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREENEGQIAPPSHLIRVEGNSHAQYV
                                                                                                                                                                                                                                                                                                                      LVVVDDDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV
                                                                                                                                                                                                                                                                                                                                               R---SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI
                                                                                                                                                                                                                                                                                                                                                                                                    RRCFEARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                              EDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPPPRGSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SCAVPSTDDYAGKYGLQLDFQQNGTAKSVTCTYSPELNKLFCQLAKTCPLLVRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSETGMDPPLSQETFEDLWSLLPDPLQTVTCRLDNLS-EFPDYP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQSTQTNEFLSPEVFQHIWDFLEQPI----CSVQPIDLNFVDEPSEDGATNKIEISMDCI
                                                                                                                                                                                                                                                                                                                                                                           RRCFEVRVCACPGRDRRTEEDNYTKKRGLKPSGK----
                                                                                                                                                                                                                                                                                                                                                                                                                              EDVNSGRHSVCVPYEGPQVGTECTTVLYNYMCNSSCMGGMNRRPILTIITLETPQGLLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GLMGN-----AVPTVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
331
356
293
362
71
296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY).

T -> S (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 777.5;
Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC (REPRESSION OF NUCLEAR LOCALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSCRIPTION ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95;
                                                                                                                                                                                     p53).
tumor types;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-BINDING)
SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                 393
                                                                                                                                                                                                                                                                                                                                                                           RELAHPPSSEPPLPKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LAADMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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Best Local S
Matches 165
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DOMAIN
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF071571; AAD34213.1; -. HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-oncogene; DNA-binding; Transcription regulation; Activator Nuclear protein; Phosphorylation; Apoptosis.

DOMAIN 1 47 ARMSCRIPTION ACTIVATION (ACIDIC).

DNA_BIND 86 273 BY SIMILARITY.

DNA_BIND 86 273 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ween the Swiss Institute of Bioinform
European Bioinformatics Institute. T
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression (By similarity).
SUBUNIT: Binds DNA as a homot.
SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of a process and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE P53 FAMILY.
313
                                                                                                                                                  310
                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                130
                                                                                                                                                                                                                                                                                                                                                                                                             85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
LOIRGRKRYEMLKKINDGLDLLENKPK
                        LPVRGRETYEMLLKIKESLELMQYLPQ 390
                                                                                                     GRDRKTEETNSTKMQ------NDAKDAKKRKSVPTPDSTTIKKSKTASSAEEDNNEVYT
                                                                                                                                  GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS------PDDELLY
                                                                                                                                                                                                     PYEPPQLGSEFTTILLSFMCNSSCMGGMNRRPILTILTLETQEGIVLGRRCFEVRVCACP
                                                                                                                                                                                                                                PYEPPQVGTEFTTVLYNEMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                          AIYKKTEHVAEVVRRCPHHQ-----NEDSAEHRSHLIRMEGSERAQYFEHPHTKRQSVTV
                                                                                                                                                                                                                                                                                                                                        PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                             TDYPGEYGEKLREQKSGTAKSVTSTYSEILNKLYCQLAKTSLVEVLLGKDPPMGAVLRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AERQMNMMCNFMDSTFNEALFNLLP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSQDTFQDLWDNVSAP----PIS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273
337
363
301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 776; DB 1;
Pred. No. 2.8e-45;
3; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
PHOSPHORYLATION (BY SIMILARITY).
ACC10EEE2F5F9CFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TIQTAALENEAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -EPPSRDGANSSSPTVPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                144
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RESULT 9 P53_PIG ID P53_PIG

STANDARD;

PRT;

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Best Local S
Matches 166
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor
                                                                                                                                                                   MOD_RES
SEQUENCE
                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                   DNA_BIND
                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00870;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF098067; AAF04620.1; HSSP; P04637; 1C26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burr P.D., Argyle D.J., "Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                              Nuclear
                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-99422034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EMEUROPEAN BIOINFORMATICS. Institute. There are no restrained by non-profit institutions as long as its content if idea and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BC1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: p53 is found in increased amounts of transformed cells. p53 is frequently mut in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression.
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
  49
                           71
                                                       14
                                                                                  11
                                                                                                               166;
                                                                                                                                                                                                                                                                                             protein;
                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                     PD002681; P53;
                           QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNT 130
                                                                              LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                          PS00348; P53;
                                                       LSQETFSDLWKLLPE
                                                                                                                                                                385
386
                                                                                                                                                                                                            318
361
304
15
                                                                                                                                                                                                                                                                   94
  -VTNWLDENPDDASRVPAP--
                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                           DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                  P53;
                                                                                                                                                                                                                                                                              Phosphorylation; Apoptosis.
45 TRANSCRIPTION ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10490836;
                                                                                                                                                                                   385
                                                                                                                                                                                                          285
349
380
316
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .J., Reid S.W.J., Nasir L.; e of the porcine p53 cDNA, and the detection of p53 expressed in vitro with a variety of anti-p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                     42862
                                                                                                                         22.6%;
                                                                                                                                                                     MW.
                                                                                                               68
                                                                                                                                                                                                                                                                                                       Transcription regulation;
                                                                                                           Score 771; DB
Pred. No. 6.6e
8; Mismatches
                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                          PHOSPHORYLATION
                                                                                                                                                                                                                       BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                    OLIGOMERIZATION
                                                                                                                                                                                PHOSPHORYLATION
                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                   A4C3D88E8DF55162
-PAATAPAPAAPAPATSWPL--SSFVPSQK 93
                                                                                                                         DB 1;
.6e-45;
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                                                                                                            124;
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Sus.
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tent is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning and chromosomal mapping of feline p53 tumor suppressor gene.";
J. Vet. Med. Sci. 55:801-805(1993).
-!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P53_FELCA
P41685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 34-354 FROM N.A.
MEDLINE-94114699; PubMed-8286534;
Okuda M., Umeda A., Watsumoto Y., Momoi Y., Watari
O'Brien S.J., Tsujimoto H., Hasegawa A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TP53 OR TKF73.
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okuda M., Umeda A., Sakai T., Ohashi T., Momc Watarī T., Goltsuka R., Tsujimoto H., Hasegav "Cloning of feline p53 tumor-suppressor gene hematopoletic tumors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last anotation update)
Cellular tumor antigen p53 (Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Lymph node;
MEDLINE-94333960; PubMed-8056458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Int. J. Cancer 58:602-607(1994).
                                                                                                                                                                                                                                                                                                                                                                            growth arrest or cell type. Involved in cell cylinter circumstances and cell type. Involved in cell cell division a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin dependent kinases. Apoptosis induction seems to be mediated either by stimulation of a procession of Bcl-2
                                                                                                                                                                                                     in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                             expression.
SUBURIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                               DISEASE: p53 is found in incr
of transformed cells. p53 is
                                                                                                                   SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRE
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Tsujimoto H., Hasegawa A.;
tumor-suppressor gene and i
                                                                                                                                                                                                                                                                                             increased amounts
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Best Local
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                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
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EMBL; D16460; BAA0397.1;
HSSP; P04637; 1DLG.
InterPro; IPRO02117; P53.
Pfam; PF00870; P53; 1.
                                                                                                  Gallus gallus (Chicken)
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  STRAIN-SPAFAS;
              SEQUENCE FROM N.A
                                           NCBI_TaxID=9031;
                                                                      Archosauria;
                                                                                     Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                      Chordata; Craniata; Vertebrata; Neognathae; Galliformes; Phasian:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 770; DB 1; 1
Pred. No. 7.7e-45;
B; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY SIMILARITY).
K -> R (IN REF. 2).
D08B43BA1BC8EB78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cion; Apoptosis.
TRANSCRIPTION ACTIVATION
BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY PRPK) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                           343
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                                                                      cebrata; Euteleostomi;
Phasianidae; Phasianinae;
                                                                                                                             p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                            362
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Matches
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oncoprotein.";
Nucleic Acids Res. 16:11383-11383(1988).
-!- FUNCTION: Acts as a tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).

DNA_BIND 87 278 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00870; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002117; P53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X13057; CAA31456.1; PIR; S02193; S02193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89083584; PubMed=3060861;
                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent klnases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BCl-2 expression (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                            146
                                                                                                                                                                         190
                                                                                                                                                                                                                              130
                                                                                                                                                                                                    86
                                                                                                                                                                                                                                                           55
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                                                                                                                                                                                                                                                                                                                                                                             169;
                                                                                                                                                                                                                                                                                                                                             11 LSP-EVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMW
                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
GRETYEMLLKIKESLELMQ 386
                                                                                                  PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                  TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 189
                                                     GRDRKADEDSIRKQQVSDSTKNGDG--TKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVR
                                                                                                                                                           PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                    LEPTEVFMDLWSMLPY---SMQQL-----PLPEDHSNWQELS----PLEPSDPPPPPP
                            GRDRKIEEENFRK-----RGGAGGVAKRAMSPPTEAPEPPK-KRVLNPDNEIFYLQVR
                                                                                   PYEPPEVGSDCTTVLYNFMCNSSCMGGMNRRPILTILTLEGPGGQLLGRRCFEVRVCACP
                                                                                                                                            AVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
                                                                                                                                                                                                     EDYGGDFDFRVGFVEAGTAKSVTCTYSPVLNKVYCRLAKPCPVQVRVGVAPPPGSSLRAV
                                                                                                                                                                                                                                                                                       PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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339
364
366
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                                                                                                                                                                                                                                                                                                                                                                                       22.5%;
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                                                                                                                                                                                                                                                                                                                                                                          Score 764.5; Pred. No. 1.7e 50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (BY SIMILARITY).
FC37D0FCDF9195B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                      1.7e-44;
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                                                                                                                                                                                                                                                           -AAAAPPPLNPP--TPPRAAPSPVVPST 85
                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     many tumor types; induces
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Indels Length

55;

Gaps

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367

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317

335

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Q29537; Q9TV78;
01-NOV-1997 (Rel
                PEAM; PF00870; P53; 1.
PRINTS; PR00386
                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Last
28-FEB-2003 (Rel. 41, Last
Cellular tumor antigen p53
                                                                                                                                                                           the
                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                         Kraegel S.A., Pazzi K.A., Madewell I "Sequence analysis of canine p53 in Cancer Lett. 92:181-186(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Setoguchi A., Sakai T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation of canine p53 cDNA and full length canine p53 protein."; Oncogene 16:1077-1084(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Leukocyte;
MEDLINE=98178696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora; 
MCBI_TaxID=9615;
                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
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 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watari T., Hasagawa
"Aberrations of p53
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95323915; PubMed-7600529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissum=spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                        send
                                                                                                                                                                                                                      in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                     expression.
SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                        growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of Apontosis Affactor expression, or by repression of Bcl-2
                                                                                                                                                                                                                                             DISEASE: p53 is found in increased amous of transformed cells. p53 is frequently
                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Acts as a tumor suppressor in many
                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through 
men the Swiss Institute of Bioinformatics and the Ev
                                                          AF060514; AAC16909.1;
AB020761; BAA78379.1;
S77819; AAB42022.1;
P04637; lOLG.
                                                                                                                         an
           PR00386; P53SUPPRESSR. PD002681; P53; 1.
 PS00348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the dog."; (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                        email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9519881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor suppressor
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Tsujimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation update)
(Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Fissipedia; Canidae;
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H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detailed
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                                                                                                                                                                                                                                                                                  similarity).
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                                                                                                                                                                                                                                                                                                                                                                                            tumor types; induces
                                                                                                                                                                                                                                                                                                                                                                                                                      exons 3-8.";
                                                                                                                                                                                                                                             wide variety or inactivat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
Canis.
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CONFLICT
CONFLICT
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Nuclear protein;
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 324
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                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                             LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSD-PMW
                                                                                                                                                                                        TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 189
ERYEMFRNLNEALELKDAQSGKEPGGSRAHSSHLKAKKGQSTSRHKKLMFKREGLDS
                      ETYEMLLKIKESLELMQYLP-----
                                            GRDRRTEEENFHKKGEPCPEPPPGSTKRALPPST---SSSPPQKKKPLDGEYFTLQIRGR
                                                                 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                     PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                  AIYKKSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAKYLDDRNTFRHSVVV
                                                                                                                                             PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                           KTYPGTYGFRLGFLHSGTAKSVTWTYSPLLNKLFCQLAKTCPVQLWVSSPPPPNTCVRAM
                                                                                                                                                                                                                                           PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
                                                                                                                                                                                                                                                                 LSQETFSELWNLLPE------NNVLSSELCPAVDELLLPESVVNWLDEDSDDAPRM
                                                                                                                                                                                                                                                                                                                                                     378
381
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                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; Transcription
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42486
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4
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39.3%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                   MEES -> MQEP (IN L -> P (IN REF. )
                                                                                                                                                                                                                                                                                                                                                                                                                         BASIC (REPRESSION OF NUCLEAR LOCALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY. OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTION ACTIVATION
                                                                                                                                                                                                                                                                                                                                                          761A718FDC93DA59
                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis
                                                                                                                                                                                                                                                                                                                                 758.5;
                                                                                                                                                                                                                                                                                                                       No.
                    -OHT--IETYROOOOOOOHOHLLQKOTSIQS
                                                                                                                                                                                                                                                                                                                        4.5e-44;
                                                                                                                                                                                                                      ATSAPTAPGP--APSWPL----SSSVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulation;
                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                               129;
                                                                                                                                                                                                                                                                                                                                                                              REF.
                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              PRPK)
                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-BINDING)
SIGNAL (POTE
                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activator;
                                                                                                                                                                                                                                                                                                                                                                                                               (BY
                                                                                                                                                                                                                                                                                                                                     381;
                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                            Gaps
                      416
 380
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P53_OHP 13
P53_O P53_O
D7 P53_O
D7 P53_O
D7 P53_O
D7 28-FE
D7 28-F
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28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
Cellular tumor antigen p53 (Tum
TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P53_ORYLA S
P79820; Q9PSU7;
01-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
NCBI_TaxID=8090;
                                                                                                                             Krause M.K., Rhodes L.D., van Beneden R.J.; "Cloning of the p53 tumor suppressor gene f (Oryzias latipes) and evaluation of mutatio exposed fish.";
                                                                                                                                                                                                                                                                                              MEDLINE=97305153; PubMed=9161419;
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                      189:101-106(1997).
        FROM
                                                                                                                                                                                                                                                                                                                                                                            N.A.
    N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD; ; Q9PSU8;
    AND
        VARIANT THR-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
annotation update)
(Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                    r gene from mutational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352
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                                                                                                                                                                    hotspots
                                                                                                                                                                                                                Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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Best Local
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H. "Isolation of cDNAs encoding the p53 tumor suppressor go Japanese Medaka (Oryzias latipes)."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases -I- FUNCTION: Acts as a tumor suppressor '----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Himedaka;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression (By similarity).
SUBUNIT: Binds DNA as a homote
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE P53 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Acts as a tumor suppressor in many
   316
                               207
                                                                                          152
                                                                                                                      196
                                                                                                                                                                                  136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF003949; AAD01195.1; -. AF003950; AAD01196.1; -. P04637; IYCS
                                                                                                                                                                                                                                                                                                                                     163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00870; P53;
                                                                                                                                                   92
                                                                                                                                                                                                                56
                                                                                                                                                                                                                                                                         14
                                                                                                                                                                                                                                             76
                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                            HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKA
DEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS-----PDDELLYLPVRG
                                            VGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKA
                                                                                                      EHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQ
                                                                                                                                                   YELELRFOKSGTAKSYTSTYSETLNKLYCOLAKTSPIEVRVSKEPPKGAILRATAYYKKT
                                                                                                                                                                                                                ---GTFDDKI---
                                                                                                                                                                                                                                        GLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGP
                                                                                                                                                                                                                                                                        FQELWETVSYP--PLETLSLPTVNEPTGSW-----VATGDMFLLDQDLS--
                                                                                                                                                                                                                                                                                                      FQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPQYTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requires a license agreement (See http://www.isb-sib.ch/announce/
                            PGSEMTTILLSYMCNSSCMGGMNRRPILTILTLET-EGLVLGRRCFEVRICACPGRDRKT
                                                                                          EHVADVVRRCPHHQ
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC60146.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                          273
331
350
295
351
91
91
22
39753
                                                                                                                                                                                                                                                                                                                                                21.9%;
                                                                                        ----NEDSVEHRSHLIRVEGSQLAQYFEDPYTKRQSVTVPYEPPQ
                                                                                                                                                                                                                                                                                                                                                                                                 WW;
                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                                            -----FDIP---IEPVPTNEVNPPPTTVPVTTDYPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homotetramer (By
                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.6e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (BY SIMIL S -> T.
MISSING (IN REF. 1).
196868866351BFF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                    Score 746.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSCRIPTION ACTIVATION (AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                  i.6e-43;
ies 92;
                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                352;
                                                                                                                                                                                                                                                                                                                                    69;
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368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P53_BOVIN STANDARD
Q29628;
01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, L
28-FEB-2003 (Rel. 41, L
                                                                                                                                       EMBL; X81704; CAA57348.1; -. EMBL; D49825; BAA08629.1; -. EMBL; U74486; AAB51214.1; -.
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=B.indicus; STRAIN=Boran; TISSUE=Blood; Bishop R.R.P., Gobright E.E.I.; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-Bovine; TISSUE-Liver; MEDLINE-95352829; PubMed-7626789;
                                                                              PIR; S51648; S51648.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                + + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida "Predominant p53 mutations in enzootic bovine leukemic over. Immunol. Immunopathol. 52:53-63(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dequiedt F., Kettmann R., Burny A., Willems L.; "Nucleotide sequence of the bovine P53 tumor-suppressor cDNA."; DNA Seq. 5:261-264(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
NCBI_TaxID=9913, 9915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-Bovine; STRAIN-Holstein; MEDLINE-96401400; PubMed-8807776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 13-386 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cellular tumor antigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of transformed cells. point many types of cancer SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression.
SUBUNIT: Binds DNA as a h
SUBCELLULAR LOCATION: Nuc
DISEASE: p53 is found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        indicus (Zebu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases Apoptosis induction seems to be mediated either by stimulation BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BELONGS TO THE P53 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p53 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a homotetramer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             increased amounts in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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InterPro;

IPR002117; P53.

PF00870; PR00386;

P53SUPPRESSR

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PS3 MAT ID PS5 MAT ID MATERIAL PS5 MATE
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Best Local Sin
Matches 152;
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DOMAIN
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DOMAIN
                                                                                                                                                  "Peritelson M.A., Ranganathan P.N., Clayton M.M., z
"Partial Characterization of the woodchuck tumor
its interaction with woodchuck hepatitis virus X
hepatocarcinogenesis.",
Oncogene 15:327-336(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                036006;
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-97376996; PubMed-9233767;
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                        Marmota monax (Woodchuck)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellular tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P53_MARMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local :
FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQQQQH-QHLLQKQTSIQSPSSYGNSSPPLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPYAQPSSTFDALSPSPA------IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTNT----SSSPQPKKKPLDGEYFTLQIRGFKRYEMFRELNDALEL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RONTHGIQMTSIKKRRSP-DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGGMNR
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                                                                                                                                                                                                                                                                                                                                                                                  Metazoa;
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1 44 TRANSCRIPTION ACTIVATION (AC 4 285 BY SIMILARITY.

3 349 OLIGOMERIZATION.

BASIC (REPRESSION OF DNA-BINT MICLEAR LOCALIZAMTON.

15 PHORMAL ACTIVATION (AC 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          annotation update)
(Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57;
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Pred. No. 8.1e
57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY R -> T (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata;
Sciurognathi; Sciurida
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No. 8.1e-43;
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                                                                                                                                                                                         , Zhang S.M.;
or suppressor,
x antigen in
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SIGNAL (POTE
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                                                                                                                                                                                                                                                                                                                                                             Sciurinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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                                                                                                                                                                                                                 p53,
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SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ001022; CAA04478.1; HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002117; P53.
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- SUBCELLULAR LOCATION: N

- DISEASE: p53 is found i

of transformed cells. F
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SIMILARITY: BELONGS TO THE
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                     408
                                          322
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en the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                  126
                                                                                                                                                                                                                                                                                                                                                                163;
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transformed cells. p53 is
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                                                                                                                                   FRHSVVVPYEDPEVGSECTTIHYNYMCNSSCMGGMNRRPILTITLEGSSGNLLGRNSFE
                                                                                                                                                  GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFE
                                                                                                                                                                                            GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT
                                                                                                   ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNT----
                                                                                                                                                                             GTRVRAMAIYKKSQHMTEVVRRCPHHE--RCSDSDGLAPPQHLIRVEGNLRAEYLDDRNT
                                                                                                                                                                                                                                      ---IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
                                                                                                                                                                                                                                                                       PMDDL-LLSSED--VENWFDK----GPDEALQMSAAPAPKAPTPAASTLAAPSPATSWPL
                                                                                                                                                                                                                                                                                    QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA-----
                                                                                                                                                                                                                                                                                                                                       LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
IFKR---EGPDS
                    LQKQTSIQSPSS
                                           DGEYFTLKIRGRARFEMFQELNEALELKDAQAEKEPGESRPHPSYLKSKKGQSTSRHKKI
                                                                 DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHT--
                                                                                        VRVCACPGRDRRTEEENFRKR-----
                                                                                                                                                                                                                           SSSVPSQNTYPGVYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQLAKTCPVQLWVDSTPPP
                                                                                                                                                                                                                                                                                                                    LSQETFSDLWNLLP-----
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                                                                                                                                                                                                                                                                                                                                                               70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription
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                                                                                                                                                                                                                                                                                                                                                              Score 738; DB 1; 1
Pred. No. 1.1e-42;
D; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                          BASIC (REPRESSION OF NUCLEAR LOCALIZATION PHOSPHORYLATION (BY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTION AGES SIMILARITY.
OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY SIMILARITY) E1DE5DB84BA40182 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
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                                                                                       -GEPCPEPPPRSTKRALPNGTSSSPQPKKKPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is produced through a collaboration - 
ormatics and the EMBL outstation -
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SIGNAL (POTENTIAL).
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Search completed: August 7, 2003, 09:47:22 Job time: 13.3675 secs

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2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_manmal:*
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Q9ue10 homo sapien
Q9ue10 homo sapien
Q99je3 rattus norv
Q9jjp6 rattus norv
Q9jjp6 rattus musculu
Q9ubv9 homo sapien
Q9plb4 homo sapien
Q75080 homo sapien
Opubvý homo sapien
Oppib4 homo sapien
O75080 homo sapien
O89097 mus musculu
O99je2 rattus norv
O9dec7 gallus gall
O9pib7 homo sapien
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OMO	Q8NHW9	4	426	36.7	1251
Q8tdy5 homo sapien	Q8TDY5	4	450	41.6	1415.5
Q8c826 mus musculu	Q8C826	11	284	٠	1418
Q9wuj0 mus musculu	Q9WUJ0	11	497		1459.5
	Q9CU77	11	514	٠	1562
Q98sw0 xenopus lae	Q98SW0	13	365	٠	1667.5
Q8tdy6 homo sapien	Q8TDY6	4	587	٠	1741
Q9jjp1 mus musculu	Q9JJP1	11	590	•	1748
	088899	11	389	51.9	1766
brac	Q8JHZ5	13	457	•	1779
mus	Q9JJP2	11	631	•	1780.5
Omo	Q9UP74	4	356	•	1801
rat	Q99JD9	11	393	•	1802
	075922		393	٠	1813
	Q9W664		641	•	1835.5
Q9p1b6 homo sapien	Q9P1B6		416	•	2077 .
O88897 mus musculu	088897		483	•	2124
Q99je0 rattus norv	Q99JE0		487	•	2164
rati	Q99JE1		470		2164
	Q9H3D2		487	٠	2185
	Q8JHZ6		588	•	2283
	Q8JFE3	13	576	٠	2297
Q99jd6 rattus norv	299ЛD6	11	461	•	2323
Bum	64M060	11	461	•	2327
homo	Q9UP26	4	461	•	2350
homo	Q9P1B5	4	461	•	2350
Q9nph7 homo sapien	Q9NPH7	4	471	71.9	2449
Q9h3p8 homo sapien	Q9нзр8	4	501		2583
Q9qwz0 mus musculu:	Q9QWZ0	11	555	•	89

ALIGNMENTS

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ID 0993D4 PRELIMINARY; PRT; 680 AA.

AC 0993D4; Q9UP28;
DT 01-MAR-2001 (TrEMBLEAL 16, Created)
DT 01-MAR-2001 (TrEMBLEAL 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLEAL 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLEAL 13, Last annotation update)
DE TA p63 alpha (Tumor protein p63).

GN P63.

OS Homo sapiens (Human).

OC EMKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ON NCBLTAXID=9606;
RN [1]
RN SEQUENCE FROM N.A.

RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Harris D., McKeon F;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Harris Scholary at 3g27-29, encodes multiple products with
RT "p63, a p53 homolog at 3g27-29, encodes multiple products with
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RT "p64, ap54, ap5
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InterPro; IPR00160; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53sUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSTE; PS00348; P53; 1.
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075195;
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Genew; HGNC:15979;
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AF124536; AAG45607.1;
AF124537; AAG45607.1;
AF124538; AAG45607.1;
AF024530; AAG42607.1;
AF075430; AAG62635.1;
BC039815; AAH99815.1;
B04637; IYCS.
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                                                         ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                       PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
      TTGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
Nuclear protein.
SEQUENCE 641 AA; 72019 MW; S
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TISSUE-Skeletal muscle;
MEDLINE-98324755; PubMed-9662378;
MEDLINE-98324755; PubMed-9662378;
Osada M., Ohba M., Kawahara C., Ishioka C., Kana Ikawa Y., Nimura Y., Nakagawara A., Obinata M.;
"Cloning and functional analysis of human p51, v functionally resembles p53.";
funct. Med. 4:839-844(1998).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
MEDLINE=20388515;
Tani M., Shimizu
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P51 isoform TAP63ALPHA (P51B
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1 - SUBCELLULAR TOCATION: NUC

1 - SIMILARITY: BELONGS TO TI

MBL; AB016073; BAA32593.1; **

MBL; AF116769; AAF43487.1; J

MBL; AF116757; AAF43487.1; J

MBL; AF116760; AAF43487.1; J

MBL; AF116761; AAF43487.1; J

MBL; AF116762; AAF43487.1; J

MBL; AF116763; AAF43487.1; J

MBL; AF116764; AAF43487.1; J

MBL; AF116765; AAF43487.1; J

MBL; AF116765; AAF43487.1; J

MBL; AF116765; AAF43487.1; J

MBL; AF116766; AAF43487.1; J

MBL; AF116766; AAF43487.1; J

MBL; AF116768; AAF43487.1; J

MBL; 
                                                                                                                      tch 99.9%; al Similarity 99.8%; 640; Conservative
1637; 1YCS.
IPR002117;
IPR001660;
IPR001660;
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K., Kawahara C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       SAM
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                                                                                                                   ; Score 3401; D
; Pred. No. 1.1e
0; Mismatches
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180

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RACE OF THE PROPERTY OF THE PR
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MEDLINE-99018225; PubMed-9799841;
Augustin M., Bamberger C., Paul D., Schmale H.;
"Cloning and chromosomal mapping of the human p5:
chromosome 3q27 and its murine homolog Ket to monosome 3q27 and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UE10;
01-MAY-2000
01-MAY-2000
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. SMART; SM00454; SAM; 1. PROSITE; PS00348; P53; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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  SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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                                                                                                                                                                                                                                                                                                                                                                                                          680 AA;
                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             76776 MW;
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13,
22,
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                   Score 3397;
Pred. No. 2.
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Query Match
Best Local
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InterPro; IPR001660; SAM.
Pfam; pF00870; p53; 1.
PKRNTS; PR00386; p53UPPRESSR.
PRODOm; PD002681; p53; 1.
SMART; SM00454; SAM; 1.
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Q99JE3;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
TAL KET alpha protein.
                                                                                                                                                                                                                                                                                                                                     STRAIN=Wistar; TISSUE=Tongue;
MEDLINE=21363378; PubMed=11470269;
Bamberger C., Schmale H.;
"Identification and tissue distribution
                                                                                                              PROSITE; PS00348; P53; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variants.";
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Rattus norvegicus (Rat).
                                                                                      SEQUENCE
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98.5%;
98.1%;
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Last annotation update)
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Score 3353; DB 11;
Pred. No. 1.4e-277;
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Q9JJP6; O1-OCT-2000 (TrEMBLrel. 1:
01-OCT-2000 (TrEMBLrel. 1:
01-OCT-2002 (TrEMBLrel. 2:
TA2 KET alpha.
    SEQUENCE FROM N.A.
TISSUE-Lingual epithelium;
Schmale H.;
Submitted (APR-2000) to the
-i- SUBCELLULAR LOCATION: N
                                                                               Oncogene
[2]
                                                                                       TISSUE-Lingual epithellum;
MEDLINE-97460723; PubMed-9315105;
Schmale H., Bamberger C.;
"A novel protein with strong homo Oncogene 15:1363-1367(1997).
                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                       NCBI_TaxID=10116;
[1]
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epithelium;
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Murinae; Rat
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EMBL; Y10258; CAB88216.1; -.
HSSP; P04637; 1YCS.
InterPro; IPR007117; P53.
InterPro; IPR0071660; SAM.
Pfam; PF00870; P53; 1.
PRLNTS; PR00386; P53sUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 680 AA; 76760 MW; //
                             O88898
O1-NOV-1998 (7
01-NOV-1998 (7
01-OCT-2002 (7
TA*p63 alpha.
Mus musculus (Mouse Eukaryota; Metazoa;
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29; Conservative
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Gremberel.
Gremberel.
                                                                                                                        PRELIMINARY;
              (Mouse)
 Chordata;
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Pred. No. 1.5e-277;
7; Mismatches 5;
   Craniata;
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    Vertebrata;
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   Euteleostomi;
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Interpro; IPR002117; P53.
Interpro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PfNTS; PR00386; P53SUPPRESSR.
PrODOM; PD002681; P53; 1.
SYART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCA
-!- SIMILARITY: BELC
EMBL; AF075436; AAC6
HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang A., Kaghad M., Gillett E., Caput D., McKeon F.; "p63, a p53 homolog at 3q27-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 680 AA; 76788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transactivating, death-inducing, and Mol. Cell 2:305-316(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR (B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98448095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p53 homolog at 3q27-29, encodes multiple products with ivating, death-inducing, and dominant-negative activit
                                                                            GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                                                                                           LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                                                                                                                               DAVRETLRQTISEPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSSETRGERVI
                                                                                                                                                                                                                   FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                       DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                 DAVRFTLRQTISFPPRDEWNDFNFDMDSRRNKQQRIKEEGE
                                                                                                                        GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGL
                                                                                                                                                                                                        FEARICACPGRDRKADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                     SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180
                                                                                                                                                                 LLYLPYRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSMQSQSSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.5%;
98.1%;
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; Pred. No. 1.
8; Mismatche
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Matches 572;
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Q9UBV9;
Q9UBV9;
01-MAY-2000 (TrEMBLrel. 1:
01-MAY-2000 (TrEMBLrel. 1:
01-CCT-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                 Nuclear P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hagiwara K., McMenamin M.G., Harris C.C.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1.
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MEDLINE-98448095; PubMed-9774969;
MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming
Yang A., Kaghad M., Wang Y., Gillett E., Fleming
Andrews N.C., Caput D., McKeon F.;
"P63, a p53 homolog at 3g27-29, encodes multiple
transactivating, death-inducing, and dominant-neg
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee L.A., Walsh P., Prater Dellavalle R.P., Targoff I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŋ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of an autoantigen associated with chronic ulcerative stomatitis: The CUSP autoantigen is a member of the p53 family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jablonska S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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P04637; 1Y
                      190
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AF124531; AAG45610.1;
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E 586 A
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PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                         TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                     PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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                                                                  TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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etazoa; Chordata; Craniata; Vertebrata; I
theria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                                                   65756 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   1.
                                                                                                                                                                                                                                                            89.1%; Score 3033; DB 4;
100.0%; Pred. No. 2.6e-250;
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                                                                                                                                                                                                                                                                                                                                   2E2F92ABF1AF8629 CRC64;
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RESULT OF PILES OF PI
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Q9P1B4;
01-OCT-2000 (TREMBLIEL 1
01-OCT-2000 (TREMBLIEL 1
01-OCT-2002 (TREMBLIEL 2
P51 isoform delNalpha.
                                                                                                                                                                                         EMBL;
                                                                                                    HSSP; P04637; 1YCS.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
                     Prodom; PD002681;
SMART; SM00454; Si
PROSITE; PS00348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=20388515; Tani M., Shimizu K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Matches 571
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075080;
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P73H.
                               SEQUENCE FROM N.A.

SEGROO M., Seki N., Ohira M., Sugano S., Watanabe M., Tac
Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tac
Tanaka T., Shinkai Y., Kato H.;

"A second p53-related protein, p73L, with high homology
Blochem. Blophys. Res. Commun. 248:603-607(1998).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

EMBL; AB010153; BAA32433.1; -.

EMBL; AB010153; BAA32433.1; -.
  InterPro;
InterPro;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Chordata; Primates;

Craniata; Vertebrata; Catarrhini; Hominidae;

Euteleostomi;

Tachibana to

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p73.";

08, 22,

Created)

586 ₽

Last sequence update)
Last annotation updat

update)

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Similarity
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                                                   MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
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Best Local Similarity
Matches 569; Conserv
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PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P55; 1.
Nuclear protein.
Nuclear protein.
SEQUENCE 586 AA; 65734 MW; 5
                                                                                                                                                                  089097 PRELIMINARY;
089097;
01-NOV-1998 (TrEMBLrel. (
01-NOV-1998 (TrEMBLrel. (
01-OCT-2002 (TrEMBLrel. 2
DN P63 alpha.
TRP63 OR P73H.
                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                SEQUENCE FROM N.A.
MEDLINE-98448095; PubMed-9774969;
Yang A., Kajhad M., Gillett E., Fleming
Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple
transactivating, death-inducing, and dominant-neg
                                                                                                                                                                                                                                                                                                                                                              610
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Pred. No. 7
                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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         dominant-negative
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Query Match
Best Local Similarity
Matches 563; Conserv
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EMBL; AB010152; BAA32432.1; -.
HSSP; P04637; 1YCS.
MGD; MGI:1330810; Trp63.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 586 AA; 65789 MW; 6
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Senoo M., Seki N., Ohira M., Sugano
Tanaka T., Shinkai Y., Kato H.;
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-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE P53 FAMILY.
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                                                                                                                 LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
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Pred. No. 4.5e-247;
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01-JUN-2001 (
01-JUN-2001 (
01-OCT-2002 (
DN KET alpha
P63;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
[1]
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ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
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InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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'- SUBCELLULAR LOCATION: NUCLEAR

'- SIMILARITY: BELONGS TO THE P53

EMBL; AJ277447; CAC37099.1; -.

HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-Wistar, TIS
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TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                 LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
                                                                                                     MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
                                                                                                                                           ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK
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                           IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
                                                                                            MNSMNKLPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
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                  IPEQFRHAIWKGILDHRQLHDFSSPPHLLRTPSGASTVSVGSSETRGERVIDAVRFTLRQ
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2 (TrEMBLrel.
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98.3%;
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Last sequence up
Last annotation
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Pred. No. 9.9e
5; Mismatches
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Sciurognathi; Muridae; Murinae; Rat
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3 FAMILY.
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RESULT 12
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OC Eukai
OC Arch
CC Alli
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RA MEDLI
RX MEDL
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Best Local S
Matches 548
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"Cloning and expression of a chick p63 gene.";
Mech. Dev. 100:105-108(2001).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; ABB045224; BAB20631.1; -.
EMBL; ABB04524; BAB20631.1; -.
HSSP; P04637; 1YCS.
Interpro; IPR01660; SAM.
Interpro; IPR01660; SAM.
Pfam; PF00870; P53; 1.
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Q9DEC7;
Q1-MAR-2001 (TrEMBLrel. 1
Q1-MAR-2001 (TrEMBLrel. 1
Q1-OCT-2002 (TrEMBLrel. 2
DN p63 alpha.
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SEQUENCE 582 AA;
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Gallus gallus (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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548; Conserv
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                            LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
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95.8%;
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Eukaryota; Metazoa; (
Mammalia; Eutheria; |
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01-OCT-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
P51 isoform TAp63beta.
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L; AF116757; AAF43488.1; JOINED.
L; AF116759; AAF43488.1; JOINED.
L; AF116769; AAF43488.1; JOINED.
L; AF116760; AAF43488.1; JOINED.
L; AF116761; AAF43488.1; JOINED.
L; AF116762; AAF43488.1; JOINED.
L; AF116763; AAF43488.1; JOINED.
L; AF116754; AAF43488.1; JOINED.
L; AF116755; AAF43488.1; JOINED.
L; AF116766; AAF43488.1; JOINED.
L; AF116766; AAF43488.1; JOINED.
L; AF116766; AAF43488.1; JOINED.
L; AF116766; AAF43488.1; JOINED.
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                                                                                                                                                                                                                                                                                       Shimizu
                                                             PQGAVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                        SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                                                                           DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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                                       PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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K., Kawahara C., Kohno
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Primates;
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Pred. No. 7.9e-224;
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Q9H3D3; Q9UD27;
01-MAR-2001 (TIEMBLITEL 1 1
01-MAR-2001 (TIEMBLITEL 1 1
01-OCT-2002 (TIEMBLITEL 2
                                                                                     ProDom; PD002681; P53; PROSITE; PS00348; P53; Nuclear protein. SEQUENCE 555 AA; 624
                                                                                                                                                                   InterPro; IPR002117; p53.
Pfam; PF00870; p53; 1.
PRINTS; PR00386; p53SUPPRESSR
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MEDLINE=98448095; PubMed=9774969;
Yang A., Kaghad M., Wang Y., Gill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                  EMBL; AF075432; AA0
HSSP; P04637; 1YCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hagiwara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrews N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "p63,
                                                                                                                                                                                                                                                    L; AF124528; AAG45608.1; JOINED.
L; AF124529; AAG45608.1; JOINED.
L; AF124531; AAG45608.1; JOINED.
L; AF124532; AAG45608.1; JOINED.
L; AF124533; AAG45608.1; JOINED.
L; AF124534; AAG45608.1; JOINED.
L; AF124535; AAG45608.1; JOINED.
L; AF124536; AAG45608.1; JOINED.
L; AF124536; AAG45608.1; JOINED.
L; AF124537; AAG45608.1; JOINED.
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                        Similarity
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1 (TrEMBLrel. 16,
2 (TrEMBLrel. 22,
79.9%; S llarity 100.0%; Conservative 0;
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                                                                                     62433 MW;
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NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE P53
    Score 2722; D; Pred. No. 8.7
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3.7e-224;
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Best Local S
Matches 503
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099JD7;
01-JUN-2001 (TREMBLEEL 1
01-JUN-2001 (TREMBLEEL 1
01-OCT-2002 (TREMBLEEL 2
                                                                                                           SEQUENCE 520
                                                                                                                                                              Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOm; PD002681; P53; 1.
PROSITE; P500348; P53; 1.
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-!- SIMILARITY: BELONGS TO THE
EMBL; AJ277452; CAC37104.1; -.
HSSP; P04637; 1YCS.
InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Wistar; TISSUE-Tongue; MEDLINE-21363378; PubMed-11470269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                              variants.";
FEBS Lett. 501:121-126(2001).
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"Identification and tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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98.4%;
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THE P53 FAMILY.
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Pred. No. 1.2e
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Search completed: August 7, 2003, 09:51:37
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AAB95136 AAB95136 ABG95142 ABF61990 ABB74990 AAB11361 AAY50997 ABP61997 ABP61997 ABP61913 ABG95134 AAB11361 ABF61914 ABG95138 ABF61914 ABG95138 ABF61914 ABG95138 ABF61914 ABG95138 ABF61914 ABG95138 ABF61914 ABG95136 ABF61914 ABG95136 ABF61914 ABG95136 ABF61914 ABG95136 ABF61914 ABG95136 ABF61914 ABG95136 ABF61914 ABF61914 ABG95136 ABF61914 ABB74989 ABB74989 ABB74989 ABB74989 ABB74989 ABB11317 ABF61869 ABF131689 ABF131689 ABB11317

Human oncogene p63
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n oncogene p63
lung cancer
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p51 protein
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ALIGNMENTS

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SO	Homo sapiens.	
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ΡI	McKeon F, Yang A;	
X		
DR	WPI; 1999-277595/23.	
DR	N-PSDB; AAX58573.	
X		

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CC cell regulatory proteins (CRPs) termed the p63 family of cell regulatory proteins (CRPs) termed the p63 family of proteins, CC which demonstrate certain sequence identity to known tumour continuous superessor proteins p53 and p73. It has been observed that the CC intron-exon organisation is conserved between p73 and p53, and from CC known exon and intron sizes for these 2 genes, it was possible to confamilifying 2 exons in a conserved domain and their intervening CC intron. The human p53 gene was localised to chromosomal position CC 3q27-29. At least 6 different isotypes exist. Splice variants CC differing at the C-terminus have been designated as alpha, beta and CC gamma forms, while p63 members differing in the N-terminus are CC designated as deltaN and TA forms, where the deltaN form lacks the CT transactivation domain. The present sequence represents human CC p63 isotype TAp63 beta. D63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes CC and induce apoptosis. Cessation or down-regulation of p63 expression CC may play a critical role in the process of cervical squamous cat as dominant negatives towards transactivation by p53 and p63. CC cachexia) and neuronal differentiation and related degenerative CC disorders. p63 polypeptides (see AAV58572-83) and anti-p63 antibodies of the invention can be used to CC identify compounds useful for treating disorders involving such CC contexis, in detection and diagnosis, and in the production of CC transgenic animals.
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                                                  GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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Pred. No. 2.2e-226;
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RESULT 2
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                                                                                                                                                  Best Local Similarity Matches 516; Conserv
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
                                                                                                                                                                                                                                    This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The poptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 255-256; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     in a
                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide comprising an immunogenic portion of a protein is used for detecting and monitoring progression of
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vaccine; detection.
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                                                                                                                                                   Conservative
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99US-0476496
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                                                                                                                                                  Score 2751; DB 21;
Pred. No. 2.2e-226;
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RESULT 3
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XX ABG95141
XX ABG9
XX ABG1

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              The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous
                                                                                                                                     Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                  01-MAR-2001; 2001US-272751P
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)B; ABS73333.
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                                Human; lung cancer;
                                                                      Human
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                                                                                                                                         ABP61915;
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                                                                      associated
                                                                                                                                                                         Protein;
                                  lung tumour;
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CC protein or cellular protein isoforms (II) dependent on heat shock CC protein (HSP)-90, or selectively treating cells expressing (II) CC involving administering HSP90-inhibitor. The method is useful for CC involving genetically-defined disease with chromosomal aberration yielding CC oncogenic fusion protein, treating cancerous cells containing fusion CC protein in heterogeneous cell population, treating proliferative disease CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. CF3), or selectively treating cells expressing mutant protein or cellular CC protein isoform in a patient heterozygous for (II). The method is useful CC protein isoform myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, CC or a disease characterised by a solid tumour such as T or B cell CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, CC or a disease characterised by a solid tumour such as papillary thyroid CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and CCC infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIWQV
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Pred. No. 2.2
); Mismatches
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2s 0;
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NO:344.

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                                                                                                                                                                                                                                                                                                                                                 The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the cotological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in the paramaceutical compositions, e.g. vaccines. (I) is useful as a marker to confide the presence or absence of a cancer such as lung cancer.

CC AB092145 to AB092486 and ABP61866 to ABP6192 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel lung carcinoma polynucleotide sequences and polypeptides ence by the polynucleotides, useful in pharmaceutical compositions such vaccines and as markers to indicate the presence of lung cancer -
                                                                                                                                                                                                                                                                                                                                                 Sequence
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07-MAY-2001;
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PD, Fanger
                                                                                                                                            FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                           MSQSTQTNEETLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
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; 2001US-0850716.
; 2001US-0897778.
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Retter MW, Durham M, Fanger GR,
Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381pp;
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                                                                                                                                                                                                                                                                                                          Score 2751; DB 23; Pred. No. 2.2e-226;
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MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ

Query Match Best Local S Matches 516

tch 100.0%; al Similarity 100.0%; 516; Conservative

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Score 2751; DB 23; Pred. No. 2.2e-226; Mismatches 0;

Length Indels

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15-SEP-2000;
09-OCT-2000;
12-DEC-2000;
                            The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49500 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                     Wang T,
McNeill
                                                                                                                                                                                         N-PSDB;
Sequence
                                                                                                                                   Example 2; Page 327-328; 374pp; English.
                                                                                                                                                       Polynucleotides encoding lung lung cancer or stimulating an
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02-AUG-2000;
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DB; ABL49252.
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Carter D, Watan
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2000US-0630940.
2000US-0643597.
2000US-0662786.
2000US-0685696.
2000US-0735705.
2001US-0850716.
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AΑ;
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immune response -
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Y, Peckham DW;
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                                                                                                                                                                                                 Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 90 HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
Treating genetically-defined disease associated with aberrations yielding oncogenic fusion proteins, e.g. \,
                                                                                               01-MAR-2001;
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                                 2002-698710/75.
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Matches 515
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                                                                                                                 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Domain
                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                         related human gene p51, useful nt of cancers and screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTSUKA PHARM CO LTD IKAWA Y.
                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                            1; Page 152-154; 163pp;
                                                                                                                                                                                                                                                                                                                                                                                                           AAZ25771
ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                            PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                  SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                           DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                       SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                               PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ikawa S,
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                                                                                                                                                                                                                                                              drugs,
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                                         The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the clintron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isotypes exist. Splice variants of differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are transactivation domain. The present sequence represents human p63 isotype TAp63 alpha. 16 James tested in a variety of thems and the present sequence represents human p63 was detected in a variety of thems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell regulatory protein; p63; huTAp63 alpha; TAp63 alpha; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
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15-OCT-1997;
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97US-0062076.
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demonstrates remarkably lity to transactivate p5
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                                                                                               Lung cand vaccine;
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                                   WO200061612-A2
                                                                                                                                               Human
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
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511; Conservative
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SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
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                                                                                             LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                                             FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
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240 180 180 120

Score 2722; DB 21; Pred. No. 9.2e-224; Mismatches

Length Indels

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This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 245-247; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide comprising protein is used for detecting an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0466396.
99US-0476496.
2000US-0480884.
2000US-0510376.
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                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                        Chimera gene of the
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PQGAVIRAMPYYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                         SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                      DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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                                                                                                            MSQSTQTNEFLSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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                                                                                                                                                                                                                                                                                                             ne of the p53 family, useful for gene therapy, and treatment comprises a transcription activating region and a DNA
                                                                                                                                                                                                                                                                                  Page 37-40;
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                                                                                                                                                      Conservative
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Pred. No. 9.2e-224;
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                    The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II)
                                                                                                                                                                                                                                                                       Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                      Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002;
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            Chromosome aberration; oncogenic fusion protein; cancer; oncogen proliferative disease; cellular protein isoform; heat shock proliferative disease; cellular protein isoform; heat shock proliferative disease; cancer; haematopoietic disorder; HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CMI acute myeloid leukaemia; AMI; chronic myelomonocytic leukaemia;
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CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC lymphoma, chronic myeloid leukaemia (CML), APL, ANL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 338-340; 389pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases,
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rhabdomyosarcoma; synovial sarcoma; viral infection.
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                                       infections. This is the amino acid sequence of a human oncogenic
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Matches Query Match Best Local

Similarity

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Score 2722; DB 23; Pred. No. 9.2e-224; Mismatches

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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arrhitis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular
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                                                                                                                                                                                                                      Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p63 isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synovial sarcoma; viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia;
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RESULT 14 ABP61910

standard;

Protein;

ABP61910 st; ABP61910; 07-OCT-2002

entry)

Human lung cancer associated

protein sequence SEQ

ID NO:339

lung

lung tumour;

cytostatic;

12-DEC-2000; 07-MAY-2001; 30-NOV-2001; , 2001WO-US47576

20-JUN-2002

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein
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           SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                                   GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                       LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLHLQKQTSIQSPSSY
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SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                     MSQSTQTNEFLSPEVFQHIWDFLEQPICSYQPIDLNFYDEPSEDGATNKIEISMDCIRMQ
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic CC activity, and can be used in gene therapy and in vaccines. Compositions CC comprising (I) or (II) can be used for stimulating an immune response in CC a patient and for treating lung cancer in a patient. Oilgonucleotides of CC (I) can be used for detecting the presence of a cancer in a patient, by CC obtaining a biological sample from the patient, contacting the sample, an CC comparing the amount of polynucleotide that hybridises to the oilgonucleotide and CC comparing the amount of polynucleotide that hybridises to the oilgonucleotide contacting the presence of a cancer in the patient. (I) and (II) are useful in CC comparing the amount of polynucleotide that hybridises to the CC presence of a cancer in the patient. (I) and (II) are useful in CC indicate the presence or absence of a cancer such as lung cancer. CC AB092145 to AB092486 and AB061866 to AB092192 represent sequences used CC in the exemplification of the present invention.
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Best Local
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McNeill PD, Fanger N, Rette
Carter D, Watanabe Y, Peckh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 328-329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer -
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                                         GNSSPELNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                     LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLLQKQTSIQSPSSY
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                                                                                                                                                FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
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Peckham DW,
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, Durham M, Fanger GR,
W, Cai F, Foy TM;
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RESULT 15
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ID ABB74
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Human
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PR 15-SH
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Best Local S
Matches 511
                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes human lung tumour proteins. Huma tumour proteins and polynucleotides have cytostatic and immunost activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies fusion proteins, T cell populations, or antigen presenting cells express the lung tumour proteins are useful for treating lung castimulating an immune response. ABL48959 to ABL49300 and ABB7494 ABB7570 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang T,
McNeill
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example
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12-DEC-2000;
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21-AUG-2000;
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Similarity 100.0%;
11; Conservative 0;
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2001US-0850716.
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2000US-063Q940.
2000US-0643597.
2000US-0662786.
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Retter MW, )
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                                                                                                                                                                                                                                             Score 2722; DB 23;
Pred. No. 9.2e-224;
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Y, Peckham DW;
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480	GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL	421	Ф
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420	LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSY	361	Db
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360	FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360	301	Db
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Search completed: August 7, 2003, 09:46:23 Job time: 37.5862 secs

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Sequence 6, Appli	Sequence 2, Appli	Sequence 32, Appl	Sequence 7, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 6, Appl1	Sequence 2, Appli	Sequence 26, Appl	Sequence 25, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 27, Appl	Sequence 2, Appli	Sequence 20, Appl	Sequence 3, Appli	

ALIGNMENTS

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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHOD
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CONTROL APPLICATION UNMBER: US/19/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 516; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                  ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
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Fanger, Gary R.
Li, Samuel X.
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Kalos, Michael D.
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Pred. No. 4e-241;
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OF LUNG CANCER
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APPLICANT: Skeig, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C9

CURRENT APPLICATION NUMBER: US/09/606,421B

CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 344

LENGTH: 516
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APPLICANT: Wang, Tongton
APPLICANT: Kalos, Micha
APPLICANT: Kalos, Micha
APPLICANT: Hosqur, Chai
APPLICANT: Hosqur, Chai
APPLICANT: Fanger, Gary
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US-09-606-421B-344
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                              FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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; SEQ ID NO 339
; LENGTH: 641
; TYDE: PRT
; ORCANISM: Homo sapiens
US-09-643-597-339
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APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Wang, Aijun

APPLICANT: Wang, Aijun

APPLICANT: Skelky, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: MCNell, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455011
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CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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Fan, Liqun
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APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

FITLE OF INVENTION: COMPOUNDS AND METHODS FO

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA

FILE REFERENCE: 210121.455C8

CURRENT APPLICATION UNMBER: US/09/542,615A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 350

COMPMEND: FORTHER OF SEQ ID NOS: 350
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SOFTWARE: FAS
SEQ ID NO 339
FNGTH: 641
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Best Local Similarity 100.
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: MAD DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT APPLICATION TOWNER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
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                                               Patent No. 6426072
GENERAL INFORMATION:
                                                                      Sequence 342,
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Best Local
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   APPLICANT:
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TYPE: PRT
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          Wang, Tongtong
Fan, Liqun
Kalos, Michael
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Chaitanya
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Pred. No. 2.4e-238;
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NT: Bangur, Chaitanya
NT: Hosken, Nancy A.
NT: Fanger, Gary R.
F INVENTION: COMPOUND
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                                                    Wang, Tongo
Fan, Liqun
                                Kalos, Michael D.
Bangur, Chaitanya
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455c11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
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Best Local Sim
Matches 510;
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SPTQALPPPLSMPSTSQCTPPPPYPTDCSIV
                                     SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511
                                                                            GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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pred. No. 1.4e-237,
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Tongtong

US/09542615A

COMPOUNDS

AND

METHODS

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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: L1. Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TILE REFERENCE: 210121.455C9
CURRENT APPLICATION UNBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
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US-09-606-421B-342
; Sequence 342, Application
; Patent No. 6531315
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 342
LENGTH: 680
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Pred. No. 1.4e-237;
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APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND ME
TITLE OF INVENTION: AND DIAGNOSIS OF LU
TITLE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,58
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369

LUNG METHODS

ODS FOR CANCER

THE

THERAPY

Skeiky, Yasır A.W Wang, Aijun

SOFTWARE: Fa SEQ ID NO 343 LENGTH: 461

FastSEQ for

Windows

Version

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; LENGTH: 680
; TYPE: PRT
; ORGANISM: HOMO:
US-09-606-421B-342
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Patent No. 64260
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Best Local Similarity
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                                                                                     Wang, Tomyo
Fan, Ligun
                                 Fanger, Gary R. Li, Samuel X.
                                                        Hosken,
                                                                  Bangur, Chaitanya
                                                                             Kalos, Michael D.
                                                                                                                                   Application
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99.8%;
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Pred. No. 1.4e
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GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Tongtong

APPLICANT: Kalos, Michael D.

APPLICANT: Kalos, Michael D.

APPLICANT: Hosken, Mancy A.

APPLICANT: Hosken, Mancy A.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FO

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG

TITLE OF INVENTION UNMBER: US/09/542,615A

CURRENT APPLICATION NUMBER: US/09/542,615A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 350
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                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-542-615A-343
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US-09-542-615A-343
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Matches 447
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                                                                                 Matches
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Best Local :
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TYPE: PRT
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                PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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Pred. No. 1.9e-207;
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Xasir A.W.
APPLICANT: Wang, Xasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRT
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michae
APPLICANT: Bangur, Chait
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                                                                                         Bangur, Chaitany
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP - 309
                                PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
                                              PVYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
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Bangur, Chaitanya
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100.0%; Pred. No. 1.9e-207;
Live 0; Mismatches 0;
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SOFTWARE: FASTSE
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo s
US-09-643-597-338
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APPLICANT: Hanger, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAL
FILE REPERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-643-597-338
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o. 6426072
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439; Conserv
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                                            PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METTILE OF INVENTION: AND DIAGNOSIS OF FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FrastSEQ for Windows Version Seq ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-542-615A-338
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                                            PYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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            LSMPSTSHCTPPPPYPTDCSIV 511
                                                                                        PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP
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Fan, Liqun
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1; Mismatches
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APPLICANY: LL, Samuer A.

APPLICANY: Wang, Aljun

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C9

CURRENT APPLICATION NUMBER: US/09/606,421B

CURRENT FILLING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 338

LENGTH: 586

TYPE: PRT

ORGANISM: Homo sapiens

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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chait
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Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Search completed: August 7, Job time : 16.2345 secs

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Minimum DB seq length: 0
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://cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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2781.719 Million cell updates/sec
Sequence 344, App
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Sequence 339, App
Sequence 342, App
Sequence 342, App
Sequence 343, App
Sequence 348, App
Sequence 338, App
Sequence 338, App
Sequence 338, App
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ALIGNMENTS

RESULT 1 US-09-735-705-344

Application US/09735705

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APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: McNeill, Patricia D.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
TYPE: PAT
ORGANISM: Homo sapiens
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Matches 516
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1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
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Fan, Liqun
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Bangur, Chaitanya S.
                                                           100.0%; Score 2751; DB 9; ilarity 100.0%; Pred. No. 1.6e-220; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 344
ENGTH: 516
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-850-716A-344
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US-09-850-716A-344
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Best Local
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APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHOD
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
FILE REFERENCE: 210121.455C15
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PQGAVIRAMPVYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                   DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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                                                                                                                                                               {\tt MSQSTQTNEFLSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ}
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Pred. No. 1.6e-220;
Mismatches 0;
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US-09-897-778-344
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 344
LENGTH: 516
TYPE: PRT
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Best Local S
Matches 516
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APPLICANT:
APPLICANT:
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APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C16
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/897,778 CURRENT FILING DATE: 2001-06-28
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mes 516; Conserv
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                           ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                PQGAVIRAMPVYKKAEHVTEVVKRCDNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
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APPLICANT: L1, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

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Fan, Liqun
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Fanger, Gary R.
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APPLICANT: Kalos, Michael D.
APPLICANT: Meneill, Patricia D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT ETLING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
CORGANISM: Homo sapiens
US-09-850-716A-339
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CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 339
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APPLICANT: Marner
APPLICANT: Fanger
APPLICANT: Vedvic
APPLICANT: Carter
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APPLICANT: Franger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
FILE REFERENCE: 210121.455C16
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RESULT 7

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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 342
LENGTH: 680
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
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CURRENT FILING DATE: 2000-12-12
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Hosken, Nancy
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SPTQALPPPLSMPSTSQCTPPPPYPTDCSIV
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McNeill, Patricia
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Skeiky, Yas
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Fan, Liqun
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APPLICANT: Kalos, Michael D.

APPLICANT: McNeill, Patricia D.

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CP

FILE REFERENCE: 210121.455C15

CURRENT APPLICATION UNMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEO ID NOS: 440

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 342

LENGTH: 680
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US-09-897-778-342
Sequence 342, Application US/09897778
Patent No. US20020147143A1
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TYPE: PRT
ORGANISM: Homo :
S-09-850-716A-342
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                      Watanabe, Yoshihiro
Henderson, Robert A
                                                 Vedvick, Thomas
Carter, Darrick
                                                                          Marnerakis, Margarita
Fanger, Gary R.
             Peckham,
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Bangur, Chaitanya (Hosken, Nancy Fanger, Gary R. Li, Samuel X.

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Wang, Aijun Skeiky, Yasir A.W. Henderson, Robert A. McNeill, Patricia D.

Neil

COMPOSITIONS AND AND DIAGNOSIS OF

METHODS FOR LUNG CANCER

THE

APPLICANT: TITLE OF II TITLE OF II

INVENTION: INVENTION: APPLICANT:
APPLICANT:

Wang, Tong Fan, Liqun Kalos, Michael D.

Tongtong

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RESULT 10
US-09-735-705-343
; Sequence 343, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 342
LENGTH: 680
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; ORGANISM: HOMO US-09-850-716A-343
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APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
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Best Local S
Matches 447
                                                                                    NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows
SEQ ID NO 343
LENGTH: 461
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                           Query Match
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    Matches
                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CIFILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
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CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.4
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TYPE: PRT
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86.5%; 500
100.0%; Pr
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  Score 2379; DB 10;
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0; Mismatches 0;
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APPLICANT: Peckham, David w.

APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-343
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APPLICANT: Marne
APPLICANT: Fange
                                                                                                                                                                  Local Similarity 100 nes 447; Conservative
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Henderson, Robert A.
Peckham, David W.
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Carter, Darrick
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Pred. No. 1.2e-189;
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APPLICANT: Fanger, Neil;
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRI
COCCANATION NUMBER: FASTSEQ FOR WINDOWS VERSION 3.0
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Hosken, Nancy
Fanger, Gary R
Li, Samuel X
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Skeiky,
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milarity 99.3%;
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Pred. No. 1.2e-185;
1; Mismatches 2;
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APPLICANT: MacNeill, Patricia D.

APPLICANT: McNeill, Patricia D.

APPLICANT: Retter, Marc M.

APPLICANT: Retter, Marc M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C15

CURRENT APPLICATION NUMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 440

SOFTWARE: FFastSEQ for Windows Version 3.0

SEQ ID NO 338

LENGTH: 586

TYPE: PRT

ORGANISM: Homo sapiens

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US-09-850-716A-338
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LSMPSTSHCTPPPPPYPTDCSIV
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                                                                    MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 489
                                                                                                             ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK
                                                                                                                                                                                                                                                                  PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
                                                                                                                                                                                                                                                                                                                           TDYPGPHSSDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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                                        {\tt MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP}
                                                                                                ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTS1QSPSSYGNSSPPLNK
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99.3%;
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Pred. No. 1.2e-185;
1; Mismatches 2;
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g

435

LSMPSTSHCTPPPPPPPTDCSIV 456

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APPLICANT: Peckham, David W.

APPLICANT: Penger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER

FILE REFERENCE: 210121.455016

CURRENT APPLICATION NUMBER: US/09/897,778

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 467

SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0

SEQ ID NO 338

LENGTH: 586

TYPE: BRT
ORGANISM: Homo sapiens

US-09-897-778-338
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; Patent No. US20020147143A1
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APPLICANT: Wang, Tongtong
APPLICANT: Warnerakis, Margarita
APPLICANT: Fanger, Gary R.
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Best Local Similarity 99.3%;
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LSMPSTSHCTPPPPYPTDCSIV 511
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                                                                                                                                             ETYEMILKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK 429
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Vedvick, Thomas S.
Carter, Darrick
Watanabe, Yoshihiro
Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2333; DB 10;
Pred. No. 1.2e-185;
1; Mismatches 2;
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Search completed: August 7, 2003, 09:57:07 Job time: 24.0296 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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A; Reference number: JH0631; MUID:92210006; PMID:1339362
A; Accession: JH0631
A; Molecule type: mRNA
A; Residues: 1-396 <DEF>
A; Cross-references: GB:N75145; NID:9213828; PIDN:AAA49605.1; PID:9213829
A; Cross-references: GB:N75145; NID:9213828; PIDN:AAA49605.1; PID:9213829
A; Experimental source: liver
C; Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement: This protein is the product of a tumor suppressor gene, p53, whose inactive cyclement is the product of a tumor suppressor gene, p53, whose inactive cyclement is the product of a tumor suppressor gene, p53, whose inactive cyclement is the product of a tumor suppressor gene, p53, whose inactive cyclement is the product of a tumor suppressor gene, p53, whose inactive cyclement is the product of a tumor suppressor gene, p53, whose inactive cyclement is the product of a tumor suppressor gene, p53, whose inactive cyclement is the product of a tumor suppressor gene, p53, whose inactive cyclement is the product of a tumor suppressor gene, p53, whose inactive cyclement is the product of a tumor s
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cellular tumor antigen p53 - rainbow trout

(c;Species: Oncorhynchus mykiss (rainbow trout)

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: JH6631

R;de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.

Gene 112, 241-245, 1992
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hypothetical prote	T26050	N	792	4.3	118	UI
hypothetical prot	T40690	N	884	4.3	118.5	**
hypothetical prot	T41011	N	513	4.3	118.5	w
hypothetical prot	T32008	Ŋ	1819	4.3	119.5	~
	184499	Ŋ	1706	4.3	119.5	,
hypothetical prot	T03908	Ņ	596	4.3	119.5	J
AF4 protein - mous	T42230	Ŋ	1211	4.4	120	Ð
hypothetical prote	S56230	N	832	4.4	120	w
hypothetical prot	T14792	N	561	4.4	120	7
dead ringer nuclea	JC6093	N	901	4.4	120.5	۱ن
hypothetical proto	T04518	N	864	4.4	122	U
hypothetical prot	н85335	N	864	4.4	122	**
hypothetical	T15446	Ŋ	969	4.5	122.5	w
SNF2alpha proteir	S45251	N	1572	4.5	123	N
castor protein	JH0797	2	799	4.5	125	_
hypothetical prot	T47149	N	724	4.5	125	ں

ALIGNMENTS

327 IYTLQIRGKEKYEMLKKENDSLELSELVPVADADKYRQK 365	В
361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 399	QY
267 PGRDRKTEEINLKKQQETTLETKTKPAQGIKRAMKEASLPAPQPGASKKT	DЬ
309 PGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQ-NTHGIQMTSIKKRRSPDDE 360	Qy
207 VPYEPPQVGSECTTVLYNFMCNSSCMGGMNRRPILTIITLETQEGQLLGRI	Ъ
249 VPYEPPQVGTEFTTVLIVNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICAC	Qy
148 LAIYKKLSDVADVVRRCPHHQSTSENNEGP-APRGHLVRVEGNQRSEYMEDGNTLRHSVL	Db
189 MPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVL	Qy
88 TSDYPGALGFQLRFLQSSTAKSVTCTYSPDLNKLFCQLAKTCPVQIVVDHPPPPGAVVRA 147	Db
129 NTDYPGPHSEDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRA 188	Qy
40 GYDNFMMEAPLQVEFDPSLFEVSATEPAPQPSISTLDTGSPPTSTVPT 87	Db
71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDALS-PSPAIPS 128	Qy
12 LSQESFEDLWSWV 39	Db
11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRWQDSDLSDPWWP 70	Qy
Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps	Matc
y Match 30.8%; Score 847.5; DB 1; Length 396;	Quer

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A29376

A29376

cellular tumor antigen p53 - African clawed frog

C;Speciles: Xenopus laevis (African clawed frog)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A29376; S61531; S72313; I51639

R;Soussi, T; de Fromentel, C.C.; Mechali, M.; May, P.; Kress, M.

Oncogene 1, 71-78, 1987

A;Title: Cloning and characterization of a cDNA from Xenopus laevis coding

A:Peference number: A29376; MUID:88143684; PMID:2830576
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F; 150, 15
F; 362/Bi
RESULT
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A; Residues: 1-51,'S',53-70,72-293,295-363 <HOW>
A; Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1;
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A; Accession: S72313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-293, 295-363 <HOE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X05191; NID:g64961; PIDN:CAR;Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                       DALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVM 177
                                                                                              R---SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI
                                                                                                                                                                                                                                                                                                  LVVVDDDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV
                                                                                                                                                             RRCFEARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKR
                                                                                                                                                                                                                                  EDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLG
                                                                                                                                                                                                                                                                              SPPPRGSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYM
                                                                                                                                          RRCFEVRVCACPGRDRRTEEDNYTKKRGLKPSGK--
                                                                                                                                                                                                            EDVNSGRHSVCVPYEGPQVGTECTTVLYNYMCNSSCMGGMNRRPILTITLETPQGLLLG
                                                                                                                                                                                                                                                                                                                                                   ----SCAVPSTDDYAGKYGLQLDFQQNGTAKSVTCTYSPELNKLFCQLAKTCPLLVRVE
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                                                                                                                                                                                                                                                                                                                                                                                                                       -----GLMGN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 777.5;
Pred. No. 9.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1e-48
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                                                                                                                                                                                                                                                                                                                                                                                                                       ----AVPTVT-
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                                                                                                                                       RELAHPPSSEPPLPKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:g64962
chel, W.
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, W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LAADMT
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Match
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cellular tumor antigen p53 - bovine
N,Alternate names: tumor-suppressor protein p53
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1
C;Accession: S51648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; E;161,164,224,280/Binding site: zinc (Cys, His, Cys, Cys) #status predict F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P. Nucleic Acids Res. 16, 11383, 1988
A;Title: Nucleotide sequence of a cDNA encoding the chicken A;Reference number: S02193; MUID:89083584; PMID:3060861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: nuclear oncoprotein p53
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S02193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S02193
A;Molecule type: mRNA
A;Residues: 1-367 <SOU>
                           A;Cross-references: EMBL:X81704; NID:9602332; PIDN:CAA57348.1; PID:9602333 (;Superfamily: cellular tumor antign p53 (C;Superfamily: cellular tumor antign p55 (C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote F;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-386 < DEQ>
                                                                                                                                                                                                                                                                  R;Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R. submitted to the EMBL Data Library, September 1994 A;Description: Nucleotide sequence of the ovine p53
  F;385/Binding site:
                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                              A; Reference number: A; Accession: S51648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYEPPQVGTEFTTVLYNFMCNSSCYGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRRRYEMLKEINEALQLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRETYEMLLKIKESLELMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYEPPEVGSDCTTVLYNFMCNSSCMGGMNRRPILTILTLEGPGGQLLGRRCFEVRVCACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEPTEVFMDLWSMLPY---SMQQL-----PLPEDHSNWQELS----PLEPSDPPPPPP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDYGGDFDFRVGFVEAGTAKSVTCTYSPVLNKVYCRLAKPCPVQVRVGVAPPPGSSLRAV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
inding site: zinc (Cys, His, Cys,
phosphoryl-RNA (Ser) (covalent)
                                                                                                                                                                                                                                            S51648
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  #status predicted
                                                                                                                                                                                                                                                                    tumor-suppressor
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cellular tumor antigen p53 - rat

Reliular tumor antigen p53 protein; nuclear oncoprotein p53

C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S02192; s41149
R;Sousei, T; de Fromentel, C.C.; Breugnot, C.; May, E.
R;Sousei, T; de Fromentel, C.C.; Breugnot, C.; May, E.
R;Sousei, T; de Fromentel, C.C.; Breugnot, C.; May, E.
R;Sousei, T; de Fromentel, C.C.; Breugnot, C.; May, E.
R;Cousei, T; de Fromentel, C.C.; Breugnot, C.; May, E.
R;Cousei, T; de Fromentel, C.C.; Breugnot, C.; May, E.
A;Reference number: S02192; MUID:89083585; PMID:3060862
A;Accession: S02192
A;MOlecule type: mRNA
A;Residues: 1-919 < SOUD-
A;Cross-references: EMBL:X13058; NID:956828; PIDN:CAA31457.1; PID:956829
R;Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A;Title: Structure of the rat p53 tumor suppressor gene.
A;Reference number: S41149; MUID:93181268; PMID:8441680
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-173, 'W', 175-391 < HUID:-
A;Cross-references: EMBL:LO7909
A;Notte: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
A;Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C;Superfamily: cellular tumor antigen p53
C;Reywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosp
F;174,177,236,240/Binding site: phosphoryl-RNA (Ser) (covalent) **status predicted
F;390/Binding site: phosphoryl-RNA (Ser) (covalent) **status predicted
                                                                                                                                                                                                                                           Matches
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Best Local :
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                                                                                           61 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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                                                                                                                                                                                                                                                                  Similarity
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SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180
                                               ----DLFLPQDV-AELLEGPEEALQVSAPAAQEPGTE-----APAPVAPASATPWPL
                                                                                                                                             SQSDMSIELPLSQETFSCLWKLL--PPDDILP-----TTATGSPNSME-----
                                                                                                                                                                                       SQSTQTNEF-LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GESRAHSSHLKSK----KRPSPSCHKKPMLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQQQQH-QHLLQKQTSIQSPSSYGNSSPPLNK 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTNT----SSSPQPKKKPLDGEYFTLQIRGFKRYEMFRELNDALEL-----KDALDGREP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQNTHGIQMTSIKKRRSP-DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPILTITLEDSCGNLLGRNSFEVRVCACPGRDRRTEEENLRKKGQSCPEPPPRSTKRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGGMNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPYAQPSSTFDALSPSPA------IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTEL
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                    26.7%; Score 735; DB 1; 38.3%; Pred. No. 1.1e-44; ative 72; Mismatches 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.88;
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57; Mismatches 94;
                                                                                                                                                                                                                                         Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380
                                                                                                                                                                                                                                                                                 Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: JH0633
R;Legros, Y; McIntyre, P.; Soussi, T.
R;Legros, Y; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992
A;Title: The cDNA cloning and immunological characterization
A;Reference number: JH0633; MUID:92210007; PMID:1555773
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C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; F;179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;395/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-396 < LEG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JH0633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 26.18;
Local Similarity 41.28;
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RDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLI/LPVRGRE
                                                                     YEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTITLEDPSGNLLGRNSFEVRICACPG
                                                                                                YEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPG
                                                                                                                                                                 IYKKLQYMTEVVRRCPHHERSSE-GDG-LAPPQHLIRVEGNMHAEYLDDKQTFRHSVVVP
                                                                                                                                                                                       DYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMP 190
                                                                                                                                                                                                                                                                                                                                                        SENVAGWLEDPGEALQGSAAAAAPAAPAAEDPVAETPAPVASAPATPWPLSSS--VPSYK
                                                                                                                                                                                                                                                                                                                                                                                                   QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRAHSSYPKTKKGQSTSRHKKPMIKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYGNSSPPLNK - - - MNSMNKLPSVSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFEVRVCACPGRDRRTEEENFRKKEEHCPELPPGSAKRALPTST----SSSPQQKKKPLD
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strain MP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 719; DB 1;
Pred. No. 1.5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 127;
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A;Molecule type: mRNA
A;Residues: 1-71,'p',73-393 <ZAK>
A;Residues: 1-71,'p',73-393 <ZAK>
A;Cross references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1;
A;Cross references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1;
R;Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
Mol. Cell. Biol. 5, 1601-1610, 1985
A;Title: Molecular cloning and in vitro expression of a cDNA clone for huma
A;Reference number: A55060; MUID:85267676; PMID:3894933
A;Accession: A55060
                                                                 A; Molecule type: mRNA
A; Residues: 1-71,'p',73-272,'H',274-393 <HAR>
A; Residues: 1-71,'p',73-272,'H',274-393 <HAR>
A; Cross-references: GB: K03199; NID: g189478; PIDN: AAA59989.1; PID: g189479
A; Experimental source: clone pR4-2, cell line A431
R; Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.;
Mol. Cell. Biol. 6, 4650-4656, 1986
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C;Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C;Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C;Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397;
4905; I58354; I78850; I52681; S60153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Human p53 cellular tumor antigen: A; Reference number: A22837; MUID:85230577; A; Accession: A22837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X01405;
R;Zakut-Houri, R.; Bienz-Tadmor,
EMBO J. 4, 1251-1255, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 3, 3257-3262, 1984
A;Title: Isolation and characterization of
A;Reference number: S42669; MUID:85126934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; R;Matlashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, EMBO J. 3, 3257-3262, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476 A;NOte: this 72-Pro allele was found in both normal and malignant cell lines R;Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R. submitted to the EMBL Data Library, August 1990 A;Reference number: S40773 A;Accession: S40773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: A variation in the A;Reference number: JT0436; A;Accession: A43073
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A;Residues: 101-393 <MKI1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-393 <C
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A; Residues: 1-71,'P',73-393 <BUC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:M22898; NID:g189474 .
A;Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-393 <BUC1>
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A;Reference number: A25224; MUID:87064416; PMID:2946935
A;Accession: A25224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-393 <LAM>
             ;Title: Molecular basis for heterogeneity;Reference number: A93086; MUID:87089826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nb, P.; Crawford, L.
Cell. Biol. 6, 1379-1385, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S42669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NID:g35215; PIDN:CAA25652.1; B.; Givol, D.; Oren, M.
             of the human PMID:3025664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequence and PMID:4006916
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PMID:6396087
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                                       p53
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                                       protein
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L.; Benchimol,
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A; Molecule type: mRNA
A; Residues: 1-189, 'LLSILSEWKEICVWSIWNTETLFDIVWWCPMSRLRLALT', 'VPPSTTTTCVTVPAWAA'
A; Cross-references: EMBL: X60010; NID: 9506432; PIDN: CAA42625.1; PID: 9506433
A; Cross-references: EMBL: X60010; NID: 9506432; PIDN: CAA42625.1; PID: 9506433
A; Cross-references: EMBL: X60010; NID: 9506432; PIDN: CAA42625.1; PID: 9506433
A; Cross-references: EMBL: X60010; NID: 9506432; PIDN: CAA42625.1; PID: 9506433
A; Cross-references: EMBL: X60010; NID: 9506432; PIDN: CAA42625.1; PID: 9506433
A; Cross-references: EMBL: X60010; NID: 9506432; PIDN: CAA42625.1; PID: 9506433
                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-247, 'Q', 249-393 <F08>
A; Cross-references: EMBL:X60017; NID:g506446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-245, 'T', 247-393 <F04>
A; Cross-references: EMBL:X60013; NID:g506438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone J6K R; Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H EMBO J. 10, 2879-2887, 1991
A;Title: p53 is frequently mutated in Burkitt's lymphoma A;Reference number: I38082; MUID:92007731; PMID:1915267 A;Accession: I38082
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k; Residues: 66-71, 'P',73-79 < MKI2>
A; Experimental source: clone lambda
A; Note: 72-Cys was also found, and
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A;Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
A;Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
R;Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, I
Mol. Cell. Biol. 7, 961-963, 1987
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A;Residues: 1-78,'T',80-393 <HAR1>
A;Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A;Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
                                       A; Molecule type:
A: Residues: 1-71,
                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A; Cross-references: EMBL: X60016; NID: 9506444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; MoLecule type: mRNA A; Residues: 1-247,'Q', 249-393 <F06> A; Residues: 1-247,'Q', 249-393 <F06> A; Cross-references: EMBL: X60015; NID: 9506442; A; Accession: I38088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-236,'I',238-393 <F05>
A;Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PID:g506441
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A; Residues: 1-71, 'P',
                                                                                                     A; Status: translated from GB/EMBL/DDBJ
                                                                                                                               A; Accession: I38090
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A; Residues: 1-393 <F03>
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A; Cross-references: EMBL: X60011; NID: g506434;
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A; Residues: 1-192, 'R', 194-393
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A; Residues: 66-79 < mKI3>
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                                                              mRNA
                                    'P',73-162,'H',164-393
      EMBL:X60018;
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164-393 <F09>
NID:g506448;
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 PMID: 3547088
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      PIDN: CAA42633.1;
                                                                                                                                                                   PIDN:CAA42632.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:CAA42630.1;
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                                                                                                                                                                                                                                                                                                                              PIDN: CAA42631.1;
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   PID:g506449
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A;Accession: I38091
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Accession: I38092
A;Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PID:g506451
A;Accession: I38092
A;Cross-references: EMBL:X60029; NID:g506452; PIDN:CAA42635.1; PID:g506453
A;Molecule type: mRNA
A;Residues: 1-253,'D',255-393 <FII>
A;Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453
A;Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 1991
A;Tatle: An Alu polymorphism intragenic to the TP53 gene.
A;Residues: 1,253,'D',255-393; MUID:g210726; PMID:1762941
A;Tatle: An Alu polymorphism intragenic to the TP53 gene.
A;Reference number: 138093; MUID:92107726; PMID:1762941
A;Accession: 138093; MUID:92107726; PMID:1762941
A;Accession: 138093; MUID:92107726; PMID:1762941
A;Accession: 138093; MUID:92107726; PMID:1762941
A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
A;Tatle: p53 gene mutations in gastric cancer metastases and in gastric cancer ce
A;Accession: A44905; MUID:92034678; PMID:1933850
A;Accession: A44905; MUID:92034678; PMID:1933850
A;Accession: A44905; MUID:92034678; PMID:1933850
A;Accession: A44905; MUID:9237829; PIDN:AAB20140.1; PID:g237830
A;Cross-references: EMBL:X54156; NID:g237829; PIDN:AAB20140.1; PID:g237830
A;Cross-references: EMBL:X54156; NID:g337829; PIDN:AAB20140.1; PID:g337830
A;Cross-references: EMBL
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 337-331, 'DQTSFQKENC' <CHO>
A;Residues: 337-331, 'DQTSFQKENC' <CHO>
A;Residues: 337-331, 'DQTSFQKENC' <CHO>
A;Ross-references: GB:S6666; NID:9436292; PIDN:AAB28601.1; PID:9436293
A;Note: mutant sequence with altered splicing and termination expressed in Mo
R;Petersen, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
MOl. Gen. Genet. 249, 425-431, 1995
MOl. Gen. Genet. 249, 425-431, 1995
A;Title: Mapping of linear epitopes recognized by monoclonal antibodies with
A;Reference number: S60151; MUID:96133682; PMID:8552047
A;Accession: S60153
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A; Cross-references: GB:S41969; NID:g1679931; PIDN:AAB19324.1;
A; Accession: I78850
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 274-277, 'S', 279-282 <HEN2>
A; Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1;
R; Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
                                                                                                                                                                                                                                                                    R;Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
A;Title: Nuclear and nucleolar target
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A; Residues: 3-44 <PET>
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                                                                                                                                                                                                                                                             Nuclear and nucleolar targeting sequences of c-erb-A, c-myb,
                                                                     11
   14
                                                                                                                                                                  Similarity
                                                          LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRNQDSDLSDPMWP
                                                                                                                                                                  26.1%;
                                                                                                                            Score 718; DB 1;
Pred. No. 1.7e-43;
9; Mismatches 132;
----NNVLSPLPSQAMDDLMLSPDDIEQWFTE--DP---
                                                                                                                                                                                              Length 393;
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58
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                                                                                                                                                                                                                                                                p53,
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A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-134,'V',136-390 <CHU>
R;Zakut-Houri, R; Oren, M; Blenz, B; Lavie, V; Hazum, S.;
Rature 306, 594-597, 1983
A;Title: A single gene and a pseudogene for the cellular tumo
A;Reference number: A02684; MUID:84068204; PMID:6646235
A;Accession: A02684
A;Molecule type: mRNA
A;Residues: 1-159,'H',161-167,'G',169-233,'I',235-390 <ZAK>
A;Cross·references: GB:X01237; GB:K01700; NID:953575
A;Cross·references: GB:X01237; GB:K01700; NID:953575
R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shoh
Mol. Cell. Biol. 6, 3232-3239, 1986
A;Title: Immunologically distinct p53 molecules generated by
A;Reference number: S38822; MUID:87064640; PMID:3023970
A;Accession: S38822
A;Molecule type: mRNA
A;Residues: 1-390 <ARA1>
A;Cross·references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1
A;Cross·references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1
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A; Title: Primary structure of DNA complementary to murine A; Reference number: S06336; MUID:88221682; PMID:3329909
A; Accession: S06336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-134,'V',136-390 <BIE>
A;Cross-references: GB:X00876; NID:g871420;
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A;Title: Analysis of the gene coding for the murine cellular A;Reference number: A22739; MUID:85027173; PMID:6092064
A;Accession: A22739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellular tumor antigen p53 - mouse
N;Alternate names: oncoprotein p53
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C;Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
                                                  A; Molecule type: mRNA
A; Residues: 1-167, 'G', 169-233, 'I', 235-390
                                                                                                               A; Accession: S38823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Chumakov, P.M.
                           A;Cross-references:
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erences: EMBL:M13873
Nomura, D.; Yokota,
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  Wolf, D.; Brill,
                                                          <ARA2>
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F;719,12,18/23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status pred
F;389/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted
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F;267-283/Region: conserved region V
F;313-319/Region: nuclear location signal
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F;108-121/Region: L1 loop
F;114-139/Region: conserved region II
F;160-192/Region: L2 loop
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A;Title: Cloning and expression analysis of full length mouse cap:Reference number: I48703; MUID:84272240; PMID:6379601
A;Accession: I48703
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A; Residues: 1-47,'R',49-78,'QW',82-390
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A; Residues: 1-167, 'G', 169-390 < ARA3>
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                                                                                                                                                                                                                                                           IKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIE--
                                                                                                                                                                                                               RDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTS
                                                                                                                                                                                                                                                                                                                                                                                                                                            --PAPATPWPLSSFVPSQKTYQGNYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDA
                                       QQQQQQHQHLLQKQTSIQS
                                                                                 PQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD----AHATEESGDSRAHSSYLKTKK 370
                                                                                                                                                                     SSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEVLCPELPPGSAKRALPTCT---SASP
                                                                                                                                                                                                                                                                                                                                                   VQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHE---RCSDGDGLAPPQHLIRVEG
                                                                                                                                                                                                                                                                                                                                                                             IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---MDDLLLPQ-----DVEEFFEGPSEALRVSGAPAAQDPVTETPGPVA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQSTQTNEF-LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQSDISLELPLSQETFSGLWKLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.1%;
38.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32-390 <RES>
NID: 953570; PIDN: CAA25323.1; PID: 953571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 717; DB 1
Pred. No. 2e-43;
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III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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R:Han, K.A.: Kulesz-Martin, M.F. Nucleic Acids Res. 20, 1979-1981, 1992 A;Title: Alternatively spliced p53 RNA in A;Reference number: S35478; MUID:92253421;

A; Cross-references: GB:M13874; NID:g200202;

PIDN:AAA39883.1;

PID: g200203

A; Molecule type: mRNA A; Residues: 1-381 <ARA>

A; Status: nucleic acid A; Accession: S35478

sequence

not shown;

not shown

transformed and PMID:1579500 translation

cells of different

A;Reference number: S38822; MUID:87064640; PMID:3023970 A;Accession: S38824

cellular tumor antigen p53, minor splice form C; Species: Mus musculus (house mouse) C; Date: 13-Jan-1995 #sequence_revision 13-Jan-19 C; Accession: S38824; S35478 R; Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Br Mol. Cell. Biol. 6, 3232-3239, 1986 A; Title: Immunologically distinct p53 molecules

13-Jan-1995 #text_change

23-Jul-1999

mouse

Brill,

. :

Shohat, þу

O.; Rotter,

۲.

alternative splicing

RESULT S38824

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A;Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; F;176,79,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predict F;392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Nucleotide sequence of a cDNA encoding the monkey A;Reference number: S06594; MUID:90045967; PMID:2530498 A;Accession: S06594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Rigaudy, P.; Eckhart, W. Nucleic Acids Res. 17, 8375,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cellular tumor antigen p53 - green monkey
C;Species: Cercopithecus acthiops (green monkey, grivet)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S06594
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A; Residues: 1-393 < RIG>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                  VRGRETYEMLLKIKESLEL
                                                                                              ACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDELLYLP
                                                                                                                                                    VVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVC
                                                                                                                                                                        VLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARIC
                                                                                                                                                                                                                                                  RAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQS 246
                                                                                                                                                                                                                                                                                                                                                                                                       QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSP----SPAI 126
:: :| :: | :: | | :| | ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                          ACPGRDRRTEEENFRKKGEPCHELPPGSTKRALPNNT---
                                                                                                                                                                                                                              RAMAIYKQSQHMTEVVRRCPHHE--RCSDSDGLAPPQHLIRVEGNLRVEYSDDRNTFRHS
                                                                                                                                                                                                                                                                                                                                            PSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSQETFSDLWKLLPE------NNVLSPLPSQAVDDLMLSPD------DLA--QW-
IRGRERFEMFRELNEALEL
                                                                                                                                                                                                                                                                                                      PSQKTYHGSYGFRLGFLHSGTAKSVTCTYSPDLNKMFCQLAKTCPVQLWVDSTPPPGSRV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                  --LTEDPGPDEAPRMSEAAPH--MAPTP-AAPTPAAPAPAPSWPLSSSV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 714.5; DB
Pred. No. 3e-43;
53; Mismatches 1:
35C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113;
                                                                          --SSSPQPKKKPLDGEYFTLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393;
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                                                                                                                                                                                        306
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158

247

127

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52

89

216

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A; Cross-references: GB:U50395; NID:q1842229; PIDN:AAC53040.1; PID:g1842230 c; Comment: This protein is a multimer, it plays the central role in a complex DNA dam iption, and recombination by protein/protein interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVR 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X90592; NID:q1532043; PIDN:CAA62216.1; PID:g1532044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor suppressor p53 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C;Accession: JCG193
R;Le Goas, F; May, P; Ronco, P; de Fromentel, C.C.
Gene 185, 169-173, 1997
                                                                                                                                                                                                                                                                                                                                         14 LSQETFSDLWKLL------PPNNVLSTLPSSDS------IEELFLSENVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 WPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                              53 WLEDSGGAL----QGVAAAAST-----AEDPVTETPAPVASAPATPWPLSSS--VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL-SPSPA----
                                                                                                                                                                                                                                                                                                        11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 AMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
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                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                            43;
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                                                                                                                                                                                                          Length 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.4%; Score 699.5; DB 2; 40.7%; Pred. No. 3.5e-42; ive 59; Mismatches 111;
                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                            61; Mismatches 116;
                                                                                                                                                                                                          ch 25.6%; Score 703.5; DB 2 1 Similarity 41.6%; Pred. No. 1.8e-42; 157; Conservative 61; Mismatches 116
                                                                                                               A;Gene: p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: liver; tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | ::| ::|||
334 GHERFKMFQELNEALEL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 GRETYEMLLKIKESLEL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity ...
...hes 156; Conservative
A; Residues: 1-393 <LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
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                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                      Best Loca
Matches
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JC6193
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                                                                  ţ
                                                                               Short known.
C'Superfamily: cellular tumor antigen p53
C'Keywords: alternative splicing; phosphoprotein; zinc
C'Superfamily: cellular tumor antigen p53
C'Keywords: alternative splicing; phosphoprotein; zinc
F;144/Domain: transcription activation #status predicted <TRA>
F;16-26/Region: conserved region I region II
F;108-121/Region: Li loop
F;108-121/Region: conserved region II
F;161-139/Region: conserved region II
F;161-139/Region: conserved region IV
F;231-252/Region: conserved region IV
F;231-252/Region: conserved region V
F;313-319/Region: nuclear location signal
F;26-283/Region: econserved region V
F;313-319/Region: econserved region V
F;313-319/Region: econserved region V
F;313-319/Region: econserved region V
F;313-319/Region: econserved region (Cys, His, Cys, Cys) #status predicted
F;79-12-18,23-37/Region: econserved region (Cys, His, Cys, Cys) #status predicted
F;713-176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;312/Relinding site: phosphate (Ser) (covalent) #status predicted
              A;Cross-references: EMBL:M13874; NID:9200202; PIDN:AAA39883.1; PID:9200203
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
C;Comment: This sequence, produced by alternative splicing of the tenth intron, lacks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :||| || |:|||||||||| :|| :|| :|| || SGUILIGRDSFEVRVCACPGRDRRTEEENPRKKEVLCPELPPGSAKRALPTCT---SASP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 RDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 LSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 IKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIE-----TYRQQQQQQH 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
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C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
C;Accession: JC6176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 SQSDISLELPLSQETFSGLWKLL------PPPED-----ILPSPHC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SQSTQTNEF-LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ---MDDLLLPQ------DVEEFFEGPSEALRVSGAPAAQDPVTETPGPVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.6%; Score 703.5; DB 2; Length 381; 38.3%; Pred. No. 1.8e-42; ive 65; Mismatches 126; Indels 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p53 cdnA
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Gene 184, 177-183, 1997
A; Title: Cloning and characterization of Chinese hamster
A; Reference number: JC6176; MUID:97183659; PMID:9031625
A; Contents: liver
A; Accession: JC6176
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor suppressor protein p53 - Chinese hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164; Conservative
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Matches 164; Conserva
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	Qy 126I	-IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPP 181	A; Introns: 30/3; 55/1; 200/2; 299/2; 327/2; 369/3; 589/3; 860/1; 986/1; 1278/1; 1547/
## Best Local S ## Watches 111 ## Watches 113 ## ## ## ## ## ## ## ## ## ## ## ## ##	06		tch 5.3%; Score 144.5; DB 2; Length 1621;
0y 3 0y 46 0y 46 0b 920 0y 80 0y 135 0y 135 0y 135 0y 133 0y 254 0y 314 0y 314 0y 318 0y 422 0y 318 0y 422 0y 365 0b 11280 0y 724 0y 365 0b 11378 Db 11280 0y 7254 0y 7254 0y 7254 0y 7254 0y 7314 0y 7254 0y 7314 0y 7254 0y 7254 0y 7314 0y 7254 0y 7314 0y 7254 0y 7316 0y 7317 0y 7318 0y 731	182		Similarity 19.6%; 1; Conservative 69
09 920 09 46 09 86 09 80 09 135 09 135 09 135 09 135 09 136 09 1378 09 314 09 314 09 314 09 318 09 3	150		3 QSTQTNEF
Ay 46 By 68 By 69 By 1028 By 135 By 133 By 128 By 133 By 138 By 141e: DNA Sy Accession: A Sy Reference nut A Sy Reference nut By A Sy Reference nut By A Sh Reference	242		920 QQTQENEEKETWKKDSRASISPKICSKDAEDATSEAVNHSTPSTSEDL
Qy 135 Qy 135 Db 1088 Qy 195 Cy 195 Cy 254 Qy 254 Qy 314 Db 1124 Qy 365 Db 1280 Qy 365 Db 1333 Qy 422 Db 1333 Qy 7422 Db 1333 Qy 625 Db 1378 RESULT 15 RESULT 15 TVFFA Protein-tyrosi C;Species: Dro C;Date: 15-Nov C;Accession: A A;Reference nu A;Recession: A A;Reference nu A;Recession: A A;Reference nu A;Recession: A A;Reference nu	302		46 968
Db 1028 Qy 135 Qy 135 Qy 195 Db 1143 Qy 254 Qy 314 Db 1124 Qy 365 Db 1280 Qy 365 Db 1333 Qy 422 Db 1333 Qy 622 Db 1378 Db 1378 Db 1378 RESULT 15 TVFFA Protein-tyrosi C; Species: Dro C; Date: 15-80 C; Date: 11-81 RESULT 15 TVFFA Protein-tyrosi C; Date: 11-81 A; Reference nu A; Residues: 1-A; Residues: 1-A; Residues: 1-A; Residues: 1-A; Residues: 1-A; Residues: 1-A; Reference nu A; Reference nu	268		80 SMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSP-AIPSNTDYPG
Db 1088 - SAAAVGSQHPMT Qy 195 AEHVTEVVKRCPN Db 1143 QPGTEGTGMTDN Qy 254 PQVGTEFTTULXN Qy 314 KADEDSIRKQQVS Qy 314 KADEDSIRKQQVS Qy 315 PVRGRETYELLK Qy 365 PVRGRETYELLK Qy 365 PVRGRETYELLK Qy 422 NSSPPLNKNSMN Db 1280 PQNGSDP Qy 422 NSSPPLNKNSMN Db 1333 SSSPS Qy 482 PTQALPPPLSMPS Qy 482 PTQALPPPLSMPS Qy 482 PTQALPPPLSMPS DD 1333 SSSPS Qy 482 PTQALPPPLSMPS A 3 SSSPS	352 326	34	1028 KMKQKTQTSDDLI 135 PHSFDVSFQQSS
Oy 195 AEHVTEVVKREPN OY 254 POWGTETTVLIN OY 254 POWGTETTVLIN OY 314 KADEDSIRKQOUS OY 314 KADEDSIRKQOUS OY 365 PVRGRETYERLLK OY 365 PVRGRETYERLLK OY 365 PVRGRETYERLLK OY 422 NSSPLNKMNSWN DD 1330 SSSPS OY 422 PTQALPPPLSWPS OY 422 PTQALPPPLSWPS OY 422 PTQALPPLSWPS OY 422 PTQALPPLSWPS OY 422 PTQALPPLSWPS OY 422 PTQALPPPLSWPS OY 422 PTQALPPPLSWPS OY 422 PTQALPPPLSWPS OY 422 PTQALPPPLSWPS OY 423 PTQALPPPLSWPS OY 423 PTQALPPPLSWPS OY 422 PTQALPPPLSWPS OY 423 PTQALPPPLSWPS OY 424 PTQALPPPLSWPS OY 425	SULT		1088 -SSAAVQSQHPMTAQSVT-PMASHIVPVAAPVPVPTFFTIPPPVPPPPPTATSTQSQ
OY 254 POVGTEETTULIND OY 314 KADEDSIRKQOVS OY 315 TGSSLEADMRK OY 365 PVRGRETYEMLLK OY 365 PVRGRETYEMLLK DD 1280 PONGSDP OY 422 NSSPPLNKMSMN OY 422 NSSPLNKMSMN DD 1333 SSSPS OY 482 PTQALPPPLSMPS Protein-tyrosine kinase (EC C, Species: Drosophila melan C; Date: 15-Nov-1984 # sequen C; Date: 15-Nov-1984 # sequence; Struth A; Reference number: A28128; A; Molecule type: DNA A; Reference number: A; Roference number: A; Reference number: A; Reference number: A; Roference number: A; Reference number: A; Roference number: A; Rof	146226 cellular tumor anti C.Species: Canis lu	gen p53 - dog (fragment) pus familiaris (dog)	195 AEHVTEVVKRCPNHELSREFNEGG : : 143 QPQFLEGLGMTDNEIVADAIRRGM
Oy 314 KADEDSIEKGOVS Oy 36 PVRGRETYEMLIK OY 36 PVRGRETYEMLIK OY 422 NSSPELNKMNSMN OY 422 NSSPELNKMNSMN OY 482 PTQALPPPLSMPS OY 482 PTQALPPPLSMPS OY 482 PTQALPPLSMPS ON 482 PTQALPPLSMPS NO. 158 PTQALPPLSMPS ON 482 PTQALPPLSMPS NO. 158 PTQALPPLSMPS ON 482 PTQALPPLSMPS NO. 158 PTQALPPLSMPS NO. 158 PTQALPPLSMPS ON 482 PTQALPS NO. 158 PTQALPPLSMPS ON 482 PTQALPS NO. 158 PTQALPS ON 482 PTQALPPLSMPS NO. 158 PTQALPS NO. 158 PTQALPS ON 482 PTQALPS ON 48	C, Date: 21-rep 1997 C; Accession: 146226 R; Devilee, P.; Van Anticancer Res 14.	sse,	254 PQVGTEFTTVLYNFMCNSSC
Oy 365 PVRGRETYERLLK OY 365 PVRGRETYERLLK Db 1280 PONGSDP OY 422 NSSPLNKMNSMN Db 1333 SSSPS OY 482 PTQALPPPLSMPS OY 482 PTQALPPPLSMPS DD 1378 PPPPLESPS RESULT 15 FYFFA Drotein-tyrosine kinase (EC C; Species: Drosophila melan C; Date: 15-Nov-1984, #sequen C; Accession: A28128; A00628 R; Hankemeyer, M.J.; Bennett Mol. Cell. Biol. 8, 483-853 A; Title: DNA sequence, stru A; Reference number: A28128; A; Molecule type: DNA A; Cross-references: GE-NIDS A; Cross-references: GE-NIDS A; Refinann, F. M.; Fresco, L. Cell 35, 393-401, 1983 A; Title: Nucleotide sequence A; Reference number: A28128; A; Cross-references: GE-NIDS A; Cross-references: GE-NIDS A; Title: Nucleotide sequence A; Reference number: A00628, A; Accession: A00628	A; Title: The canine A; Reference number:	p53 gene is subject to somatic mutations in thypoid carcinoma. I46226; MUID:95150524; PMID:7847847	314 KADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYL
Qy 365 PVRGRETYEMLLK Db 1280 PQNGSDP QY 422 NSSPELNKMNSMN QY 482 NSSPELNKMNSMN A82 PTQALPPPLSMPS QY 482 PTQALPPPLSMPS QY 482 PTQALPPPLSMPS QY 482 PTQALPPPLSMPS A82 PTQALPPPLSMPS A92 PTQALPPPLSMPS A93 PTQALPPPLSMPS A94 PTGALPPPLSMPS A94 PTGALPPPLSMPS A94	A; Accession: 146226 A; Status: prelimina	ry; translated from GB/EMBL/DDBJ	1224
0y 422 1; 0b 1333 0y 482 253 RESULT 15 TYFFA Protein-tyrosi C;Species: Dro C;Date: 15-Nov C;Accession: A R;Henkemeyer, MOI. Cell. Bio A;Title: DNA S A;Reference nu A;Accession: A A;Molecule typ A;Rediues: 1-A;Cross-reference A;Hoffman, Fr C;All 35, 333-4 A;Hoffman, Fr C;All 35, Accession: A A;Accession: A A;Access	A; Residues: 1-77 <d A; Cross-references: C; Genetics:</d 	EVS EB: L27630; NID:g508454; PIDN:AAC37327.1; PID:g508455	365 1280
253 59	533 ii	/3 ular tumor antigen p53	422 NSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLS:
	Query Match Best Local Simila Matches 47; Co	59.5, DB 2; Length 77; o. 6.5e-12; atches 14: Indels 1: Gaps	1333
·		25	1378 P
	254	271	112)
	09		C.Species: Drosophila melanogaster C.Date: 15-Nov-1984, #sequence_revision 30-Sep-1989 #text_change 11-Jun-1999 C.Arcesion: A28128: A00628
·	RESULT 14 115264		R:Henkemeyer, M.J.; Bennett, R.L.; Gertler, F.B.; Hoffmann, F.M. Mol. Cell. Biol. 8, 843-853, 1988 A:Title: DNA sequence, structure, and tyrosine kinase activity of the Drosophila mela
	nypothetical protei C;Species: Caenorha C;Date: 20-Sep-1999	n FS9E12.9 - Caenorhabditis elegans bditis elegans #sequence_revision 20-Sep-1999 #text_change,20-Sep-1999	A; Reference number: A28128; MUD:88174728; PMID:2832740 A; Accession: A28128 A; Molecule type: DNA
ree of c. eregans Cosmid FJFLI. A; Title: Nucleotide A; Reference number: A; Reference number: A; Accession: A00628	R; Johnson, D. submitted to the EM	BL Data Library, May 1997	A; RESIGUES: 1-12.0 < HEN> A; Cross-references: GB:M19692; GB:M18402; NID:g158598; PIDN:AAA28934.1; PID:g158600 R; Hoffmann, F.M.; Fresco, L.D.; Hoffman-Falk, H.; Shilo, B.Z.
ranstared from GB/EMBL/DDBJ	A; Reference number: A; Accession: 115264	218318	Cell 3) 593-401, 1930. A; Title: Nucleotide sequences of the Drosophila src and abl homologs: conservation an A; Reference number: A00628; MUID:84082064; PMID:6317185
A; Molecule type: DNA A; Resides: "A', 375, AQ', 378-644, 'VGDV' A; Resides: "A', 375, AQ', 378-644, 'VGDV' A; Resides: "A', 375, AQ', 378-644, 'VGDV' A; Resides: "C', 375, AQ', 378-644, 'VGDV'	A, Wolcaula, Prefittingford, A, Molecula type: DNA A; Residues: 1-1621 AJCTOSS-references: EMBL	.ams.raceu ilom es/Embi/Dibbo :AF003386; NID:92088833; PID:92088843; PIDN:AAB54259.1;	A;ACCESSION: AUUD.28 A;Nolecule type: DNA A;Residues: 'A',375,'AQ',378-644,'VGDV' <hof> A;Cross-references: GB:K01042; NID:g157175; PIDN:AAA28443.1; PID:g157176</hof>
C;Genetics: A;Gene: abl A;Cross-references: FlyBase:FBgn0000017 A;Introns: 112/1; 130/1; 310/2; 449/1; 6	A; Experimental sour C; Genetics: A; Gene: CESP:F59E12 A; Map position: 2	ce: strain Bristol N2; clone F59El2	

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C; Superfamily: Drosophila protein-tyrosine kinase abl; protein kinase homology; SH2 home C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transforming F F; 211-260/Domain: SH3 homology <SH3>
F; 211-360/Domain: SH3 homology <SH2>
F; 316-646/Domain: SH2 homology <SH2>
F; 386-646/Domain: protein kinase homology <KIN>
F; 394-402/Region: protein kinase ATP-binding motif
F; 417/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  973 ------ATAPSLPPANGHATPPAARLN----PKASP-IPPQQMIRSNSSGGVTMQNN 1018
                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                 929
                                                                                                                                                                                                                                                                                                                                                                                                                                         NANATSASSSAPSTSGVATGGGATTTTAASGCASSSSATASLSLTPQMVKKGLPGGQALT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 QGAVIRAM -- PVYKKAEHVTEVVKRC -----PNHELSREFNEGQIAPPSHLIRVEGNS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           820 ETDPAADPDTDATGDSLEQSLSQVIAAPVTNKMQHSLHSGGGGGGGGGPRSSQQHSSFKRP 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      880 TGTPVMGNRGLETR-------OSKRSOLHSQAPGPGPPSTQPHHGNNGVVTSAH 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 QHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQ----RNALTPTTIPDG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AGDMNGLSPTQA----LPPPLS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNTDYPGPHSFDVSFQQSSTAKSATWTYSTELK-----KLYCQIAKTCPIQIKVMTPPP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 HAQYVEDPITGRQSVLVPYEPPQV-GTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DG-QVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQN----TH 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 GIOMTSIKKRRSPDDELLY--LPVRGRETYEMLLKIKESLELMOYLPQHTIETYRQQQQQ 402
                                                                                                                                                                                                                                                                                              PICSVQPIDL-----NFVDEPSEDGAINKIEISMDCIRMQDSDLSDPMWPQYINLGLL 78
                                                                                                                                                                                                                                                                                                                                         PGCPPEVYDLMRQCWQWDATDRPTFKSIHHALE-----HMFQESSITEAVEKQ-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.1%; Score 140; DB 1; Length 1520; Best Local Similarity 21.2%; Pred. No. 0.13; Matches 120; Conservative 71; Mismatches 230; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                            NSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSP----
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Search completed: August 7, 2003, 09:53:22 Job time : 19.268 secs

OTARU) XNAJB 39A9 SIHT

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 7, 2003, 09:32:13; Search time 9.15074 Seconds (without alignments) 2651.784 Million cell updates/sec Run on:

US-09-538-106-14
2751
1 MSQSTQTNEFLSPEVFQHIW......HCTPPPPYPTDCSIVRIWQV 516 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

127863 Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ription	P73_HUMAN 015350 homo sapien	CERAE 09xsk8 cerco	ONCMY P25035	BARBU 09w678	3_BRARE	3_ICTPU	P07193	629M60	Q9tub2	P41685		Q29537		Q29628		P10361	0	_TUPGB Q9ttal	P51664	MESAU	PLAFE	P53_HUMAN P04637 homo sapien	P02340 mus r	P56423	CERAE	_MACMU P56424	_хірне	_XIPMA 092143	CRIGR 009185	095330	_SPEBE Q64662	
	DB	1			1																												•
	Length	636	637	396	369	373	376	363	367	386	386	367	381	352	386	391	391	391	393	382	396	366	393	390	393	393	393	342	342	393	391	314	
· æ	Query	53.2	53	30	29.8	5	28	28	28	28	28	27	27	27	56	26	56	26	56		56	26	26	26	56	26	25	25	25	25			
	Score		1457.5	847.5	819.5	805.5	795	777.5	176	771	770	764.5	758.5	746.5	740	738	735	732.5	730	729	719	718	718	717	715.5	714.5	713.5	710.5	709.5	707.5	699.5	969	
;	Result No.	1	7	m	4	5	ø	7	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	•

	Ogroi7 mus musculu Ognrj4 homo sapien				
ABL_DROME GALY_YEAST	ZAP3_MOUSE TUSP_HUMAN	TLE4_MOUSE	TLE4_HUMAN V70K_TYMV	V70K_TYMVA STUA_EMENI	KI67_HUMAN
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1520	1386 1544 628	766	766 628	628 590	3256
5.1	444	7.4	4.7	4.4 6.6	4.6
140 135.5	134.5	129.5	128.5	126.5	126
34 35	36 37	0 K 4	4142	4 4	45

ALIGNMENTS

SULT 1 3_HUMAN P73_HUMAN S	AC 015350; 015351; QSMTKB; DT 16-0CT-2001 (Rel. 40, Created) DT 16-0CT-2001 (Rel 40, Tast equippe undate)	15-SEP-2003 Tumor protei	DE protein). GN TP73 OR P73.	s (Human). Metazoa; Chordata;	Primates;		_	RX MEDLINE=97433090; PubMed=9288759; RA Kaghad M., Bonnet H., Yang A., Creancier L., Biscan JC., Valent A.,	Minty A., Chalon P., Lelias JM., Dumont X., Ferrara P., McKeon F	<pre>Caput D.; "Monoallelically ex</pre>	frequently deleted in neuroblastoma and other h	RL Cell 90:809-819(1997). RN [2]		KX MEDLINE-99289209; PuDMed-10362363; RA Yoshikawa H., Naqashima M., Khan M.A., McMenamin M.G., Haqiwara K.,	Harris C.C.;	RT "Mutational analysis of p73 and p53 in human cancer cell lines.";			RX MEDLINE=98389621; PubMed=9721206; RA Mai M. Huang H. Reed C. Olan C. Smith T.S. Alderete R	Jenkins R., Smith D.I., Liu W.;	"Genomic organization and mutation	RT oligodendrogliomas with chromosome 1 p-arm deletions.";			RC · TISSUE=Neuroblastoma; RX MEDLINE=99021697; PubMed=9802988;	De Laurenzi V., Costanzo A., Barcaroli D.,	RA Annicchiarico-Petruzzelli M., Levrero M., Melino G.;	Two new p/3		[5]		RX MEDLINE=99310938; PubMed=10381648; RA De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G.,	Costanzo A., Levrero M., Knight R.A.;	and identification of two new splicing variants epsilon and zeta.	
24 PT	A D C	900	ΔÖ	00	00	2 22	~	K K	24	K K	2	α: α	202.1	* *	24	PK 0	K 04	24	PX D2	4 24	. 12	מא	4 24	04 I	* *	æ	DC C	2	24 (nz c	4 24	PK PK	ρς ρ	4 64	

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FRANSFAC; T04931;
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PDB;
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DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.

DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER, APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN SURROBLASTOMA AND OLIGODENDROGLIOMA.

SEMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                 PHÓSPHORYLATION (ISOFORMS ALPHA AND BETA).
MEDLINE-99318135; PubMed-1039121;
Yuan Z.-M., Shloya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
Kharbanda S., Weichselbaum R., Kufe D.;
"p73 is requilated by tyrosine kinase c-Abl in the apoptotic response
to DNA damage.";
Nature 399:814-817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL TYROSINE KINAGE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA SUBCELLULAR LOCATION: ALPHA, AND HOMOTYPICALLY.

SUBCELLULAR LOCATION: Nuclear.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOId=015350-7; Sequence=VSP_006538; ISOId=015350-7; Sequence=VSP_006538; IISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER, SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=015350-3; Sequence=VSP_006540, VSP_006541; Note=The splicing of exon 11 results in a frameshift from the original reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isoi-015350-5; Sequence-VSP_006544, VSP_006545; Note-The splicing of exon 11 results in a frameshift from the original reading frame. The splicing of exon 13 reverts the reading frame to the sequence of isoform Alpha;
                                                                                                                                                                                                                                                                                                                                                                  н.
                                                                                                                                                                                                                 3
                                                                                                                                                                                                              Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., .:
Kharbanda S., Weichselbaum R., Kufe D.;
Nature 400:792-792(1999).
                                                        Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=015350-4; Sequence=VSP_006542, VSP_006543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event-Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=015350-2; Sequence=VSP_006539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=015350-6; Sequence=VSP_006546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=015350-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                             "The emerging p53 gene family.";
J. Natl. Cancer Inst. 91:594-598(1999).
Cell Death Differ. 6:389-390(1999),
                            SEQUENCE FROM N.A. (ISOFORM KAPPA).
                                                                                                                                                                                                                                                                                  MEDLINE-99217940; PubMed-10203277;
                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF 439-506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Epsilon;
                                                                                                                                                                                                                                                                                               Kaelin W.G. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name-Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Delta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Мате≃Карра;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name-Zeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN.
                                                                                                                                                                                                                                                                      FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPE
SYRWIYWREAUDDLKQGDENSSYAQLLASSNAATISIGGSGE
LQRQRVWEAVHFRYHTITIPNRGGPGGGDEWAPFEFDLP
DCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
MEDIATES OLIGOMERIZATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Transcription regulation; Activator; DNA-binding; Anti-oncogene; Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY ABL) (IN ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-BINDING (POTENTIAL)
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ProDom; PD002681; P53; 1.
                                                                                           EMBL; Y11416; CAA72220.1; -. EMBL; Y11416; CAA72221.1; -. EMBL; Y11416; CAA72219.1; -.
                                                                                                                          AF077628; AAC61887.1;
AF077616; AAC61887.1;
AF077617; AAC61887.1;
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AAC61887.1;
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AAC61887.1;
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AAD39696.1;
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AAD39696.1;
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Pfam; PF00536; SAM; 1.
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304
435
171
486
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                                                           MAQSTAT----SPDGGTTFEHLWSLEP------DSTYFDLPQSSRGNNEVVGGTDSS
                                                                                     MDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQP
                                                                                                                               SSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQ
                                                                                                                                                                            IKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSH
                                                                                                                                                                                                                       AQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDG
                                                                                                                                                                                                                                    QVLGRRCFEARICACPGRDRKADEDSIRKQQV -- SDSTKNGDGTKRPFRQNTHGIQM -- T
                                                                                                                                                                                                                                                                              SIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQHQHLLQ
                                                                                                                                                                                                                                                                                                                         KQTSIQSPSSYGNSSPPLNKMN-SMNKLPSVSQLIN--PQQRNALTPTTIPDGMGANIPM
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                       Gaps
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TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecus aethlops (Green monkey) (Grivet).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                     51;
  636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor protein p73 (p53-like transcription factor) (p53-related
                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                   MGTH----MPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                       114; Indels
Score 1464.5; DB 1;
Pred. No. 4.1e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
TISSUE-Kidney;
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                     60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               637
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53.2%;
         Local Similarity 57.4 les 303; Conservative
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Q9XSK8; Q9TSQ9;
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TP73 OR P73.
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                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; Activator; DNA-binding; Anti-oncogene;
Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
VARSPLIC 495 637 SFINGLGENOCIENTROSCHOOLINESTRIDELGALKIPE
OYRMATINGLIQDIKGGHOYGAAQQLLRSSNAAAISIGGSG
ELQRQRWBAVHFRVRHITIPNRGGGAGDEWAADFGFDL
PDCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVLGRRCFEARICACPGRDRKADEDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSQSTQTNEFLSPE---VFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKI----EIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 MDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 MDVFHLEGMTTS-----VMAQFNLLSSTMDQMSSRAASASPYTPEHAA-SVPTHSPYAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 IKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDG
                                                     DOMAIN THAT BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                        CENTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                        Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTId-VSP_006537.
7CB200B919C9C70A CRC64;
                                        DOMAIN,
                       ISOId=09XSK8-2; Sequence=vSP_006537;
-!- DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAI BINDING DOMAIN AND A C-TERMINAL OLICOMERIZATION TO THE ABL TYROSINE KINNSE SH3 DOMAIN.
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1457.5; DB Pred. No. 1.2e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61; Mismatches
IsoId=Q9XSK8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                 PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69630 MW;
                                                                                                                                                                                                                  EMBL; Y11419; CAA72224.1; -.
EMBL; Y11419; CAA72225.1; -.
HSSP; 015350; ICOK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.0%;
57.0%;
                                                                                                                                                                                                                                                                                                                                                SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                          InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301; Conservative
                                                                                                                                                                                                                                                                                       Pfam; PF00870; P53; 1.
Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                               SMART; SM00454; SAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     637 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103
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Best Local
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us-09-538-106-14.rsp

Thu Aug

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Nuclear protein; Phosphorylation; Apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyprinidae; Barbu
NCBI_TaxID=40830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P04637
                                                                                                                                                                                                                                                                                                                                                                                                                      TP53 OR P53
                                                                                                                                                                                                                                                                                                                                        P53_BARBU
Q9W678;
                                                                 88
                                                                                                                                             249
                                                                                                                                                                     207
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                                                                                                                                                                                                                                                361
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                                                                                                                                                                                                                                                                                                                             P53_BARBU
                                                                                                                                                                                                                                                                                                                RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39
                                                                                                                                                                                                                                                                                                                                    growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                    MEDLINE-92210006; PubMed-1339362; de Fromentel C.C., Padkel F., Chapus A., Baney C., May P., Soussi T.; "Rainbow trout p53: cDNA cloning and biochemical characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSQESFEDLW-----SWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDALS-PSPAIPS
                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
842225076545AIC CRC64;
                                                                                                                                                                               Oncorhynchus mykiss (Rainbow trout) (Salmo gairdner1).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Actinopterygii; Neopterygii; Teleostai; Euteleostai;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DNA-binding; Transcription regulation; Activator;
In; Phosphorylation; Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTION ACTIVATION (ACIDIC)
 511
                BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 396;
 MGTH----MPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                                                                                                                                                                                                                                                                                                                                                                                                               expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102; Indels
                                                                                                                                                      Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2e-50;
                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%; Score 847.5; 45.4%; Pred. No. 6.2
                                                                                         396
                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43966 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M75145; AAA49605.1; -. PIR; JH0631; JH0631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                              Gene 112:241-245(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325
369
303
395
396 AA;
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID-8022
                                                                                                                  01-MAY-1992
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181;
                                                                                         P53_ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA_BIND
DOMAIN
467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
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                                                                             P53_ONCMY
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                             248
                                                                                                                                                                                                                                                                                       266
                                                                               NTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRA 188
                                                                                                                                                          TSDYPGALGFOLRFLOSSTAKSVTCTYSPDLNKLFCOLAKTCPVQIVVDHPPPPPGAVVRA 147
                                                                                                                                                                                                                                                                                                                                                                                                       VPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICAC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGRDRKADEDSIRKQQ---VSDSTKNGDGTKRPFRQ-NTHGIQMTSIKKRRS----PDDE 360
87
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"Evolutionary conservancy of p53 gene sequences in fish.";
"Evolutionary conservancy of p53 gene sequences in fish.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
-----VEFDPSLFEVSATEPAPOPSISTLDTGSPPTSTVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                            MPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbus barbus (Barbel).
Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Barbus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-oncogene; DNA-binding; Transcription regulation; Activator;
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SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | :||:| |||| | :|||| : :| : |||:
IYTLOIRGKEKYEMLKKFNDSLELSELVPVADADKYRQK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
    40 GYDNF----MMEAPLO-
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                                                                                                                                                                                                                                                                   84 QIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSF 142
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                                                                                                                                                                                                                                                                                                        322
                                                                                                                                                                                                                                                                                                                                                                      256 DQ---ETKTLDKIPSANKRSLIKDSTSSVPRPEGSKKAKLSGSSDEEIYTLQVRGKERYE 312
                                                                                                                                                                                                                 323 QQVSDSTKNGD----GTKRPF-RQNTHGIQMTSIKKRR----SPDDELLYLPVRGRETYE 373
                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Winge P.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-! FNUCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling as set of genes required for this process. One of the activated genes is an inhibitor of cyclin dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
                                                                                                                                                                                                                                                                                                                    143 QOSSTAKSATWIYSIELKKLYCQIAKICPIQIKVMIPPPQGAVIRAMPVYKKAEHVTEVV
                                                                                                                                                                   VLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97344388; PubMed-9200835; Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z.; Bradford C.S., Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.; Zebrafish (Danio rerio) P53 tumor suppressor gene: cDNA sequence and expression during embryogenesis.";
                                                                                                                                                                                                                                                    203 KRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTT
                                   BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
OBE2CF2CEA74C304 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                            Gaps
TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                   DB 1; Length 369;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P53_BRARE STANDARD; PRT; 373 AA. P79734; 090440; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                           87;
                                                                                                               ; Pred. No. 4.3e-48; 49; Mismatches 87
          BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                  29.8%; Score 819.5; 51.2%; Pred. No. 4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6:88-97(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                         || || :|||| :| :: |||:
MLKKINDSLELSDVVPPSEMDRYRQK 338
                                                                                                                                                                                                                                                                                                                                                                                                          374 MLLKIKESLELMQYLPQHTIETYRQQ 399
                                                                          41233 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 140-212 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .. Mar. Biol. Biotechnol.
                                                                                                            Best_Local Similarity 51.2
Matches 167; Conservative
28
256
329
365
368
          66
298
342
276
368
369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TP53 OR DRP53
                         DOMAIN
DOMAIN
DOMAIN
MOD_RES
SEQUENCE
                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                      263
           DNA_BIND
                                                                                                   Query Match
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
P53_BRARE
FFFFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILJIVTLETR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 QRANYREDNITLRHSVFVPYEAPQLGAEWTTVLLNYMCNSSCMGGMNRRPILTITLETQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGOVLGRRCFEARICACPGRDRKADEDSIRK-QOVSDSTKNGDGTKRPFRONTHGIOM --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 EGQLLGRRSFEVRVCACPGRDRKTEESNFKKDQETKTWAKTTTGTKRSLVKESSSATLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
AC7AB724FA6B61FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 --TSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                           BASIC (REPRESSION OF DNA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.3%; Score 805.5; DB 1 53.9%; Pred. No. 3.8e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Mismatches
SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE P53 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ictalurus punctatus (Channel catfish).
                                                                                                                                                                                                                                                    EMBL: U46693; AAA97408.1; -.
HSSP: P04637; 1TUP.
ZFIN; ZDB-GENE-990415-270; tp53.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-99071979; PubMed-9854815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41899 MW;
                                                                                                                                                                                                                                EMBL; U60804; AAB40617.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345
280
272
373 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P53_ICTPU
093379;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
SEQUENCE
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Matches
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AC 0933_T
AC 0933_T
DT 16-0C
DT 26-PE
DE Cellu
CELKAT
OC EUKAT
OC ACLIC
OC ACLIC
OC ACLIC
OC NCBI
RN (1)
RN (1)
RN MEDDI:
RA LUFL
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Cellular tumor antigen p53 (Tumor suppressor p53)
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DNA_BIND
DOMAIN
DOMAIN
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 SDMLQPQSS--SSPPTSTVPVTSDYPGLINFTLHFQESSGTKSVTCTYSPDLNKLFCQLA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 KTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQ 347
        comp. Blochem. Physiol. 120B:675-682(1998).
- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORILATION (BY SIMILARITY).
1B89CD98DB3289F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
"Identification and characterization of the tumor suppressor p53 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 MTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 399
                                                                                                                                                                                                                                                                                                                                                                           Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein; Phosphorylation; Apoptosis.
1 36 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 376;
                                                                                                                                  expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2e-46;
                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 07, Created)
(Rel. 07, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.9%; Score 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                            InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SQPPRESSR.
ProDom; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                        EMBL; AF074967; AAC26824.1; -. HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41989 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        303
347
286
275
375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P53_XENLA
P07193;
01-APR-1988 (
01-APR-1988 (
28-FEB-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156;
                                                                                                                                                                                                                                                                                                                                                                                                              ONA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94134403; PubMed-8302570;
Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.;
Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.;
Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.;
Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.;
Hoever M., Mid-type p53 interferes with normal development
in Xenopus laevis embryos.";
Oncogene 9:109-120(1994).
I. FUNTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
BAX and FAS antigen expression, or by repression of BcI-2
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
THOSPHORYLATION (BY SIMILARITY).
THOSPHORYLATION (BY SIMILARITY).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 81; Gaps
                                                                                                                                                                                                                                                                                 Soussi T., de Fromentel C.C., Mechali M., May P., Kress M.;
Kloning and characterization of a cDNA from Xenopus laevis coding
for a protein homologous to human and murine p53.";
Oncogene 1:71-78(1987).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; Pruub, v., r., r., promote, protein, prosphorylation, Apoptosis.

Nuclear protein; Phosphorylation; Apoptosis.
TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.3%; Score 777.5; DB 1; Length 363; 42.5%; Pred. No. 2.8e-45; Live 55; Mismatches 95; Indels 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CE1F3E58F020D74D CRC64;
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OLIGOMERIZATION.
                                                                                                                                                                                                                                                       MEDLINE-88143684; PubMed-2830576;
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EMBL, XO5191; CAA28821.1; -.
EMBL, X77546; CAA54672.1; -.
EMBL, S68353; AAC60746.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 28.3%
Best Local Similarity 42.5%
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A29376; A29376.
HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
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                                                                                                       Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362
52
71
296
363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                           SPPPRGSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYM 181
                      58 RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTF. 117
                                                                   118 DALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVM 177
                                                                                                                                                                EDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLG 297
                                                                                                                                                                                                            RRCFEARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKR 354
                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSETGMDPPLSQETFEDLWSLLPDPLQTVTCRLDNLS-EFPDYP------LAADMT
                                                                                                                                                                                                                          -----AVPTVT-
                                                                                                                 178 TPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression (By similarity).
SUBGUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TQ THE P53 FAMILY.
                                                                                                                                                                                                                                                           R---SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 393
                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
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                                                                                                                                                                                                                                                                                                                                            367
                                             53 VLQE-----GLMGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon miurus (Congo puffer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF071571; AAD34213.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=94908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                              TP53 OR P53
                                                                                                                                                                                                                                                                                                                                           P53_TETMU
Q9W679;
                                                                                           89
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P53_TETMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS-----PDDELLY 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRDRKTEETNSTKMQ-----NDAKDAKKRKSVPTPDSTTIKKSKTASSAEEDNNEVYT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 QYTNLGLL-NSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LSQDTFQDLWDNVSAP----PIS----TIQTAALENEAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 AERQMNMMCNFMDSTFNEALFNLLP-------EPPSRDGANSSSPTVPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99422034; PubMed=10490836;
Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
"Nucleotide sequence of the porcine p53 cDNA, and the detection of
recombinant porcine p53 expressed in vitro with a variety of anti-p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncogene 18:5005-5009(1999).
                                                                                                                                                                                                                                       BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
Sus.
                                                                 DNA-binding; Transcription regulation; Activator;
                                                      Anti-oncogene; DNA-binginy; Alemoster Apoptosis.
Nuclear protein; Phosphorylation; Apoptosis.
TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY SIMILARITY).
ACC10EEE2F5F9CFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 3.6e-45;
53; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p
                                                                                                                                                                          BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.
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313 LQIRGRKRYEMLKKINDGLDLLENKPK 339
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 LPVRGRETYEMLLKIKESLELMQYLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequ
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                             41266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 165; Conservative
ProDom; PD002681; P53; 1
PROSITE; PS00348; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD:
                                                                                                                                                                  86
308
342
342
288
366
367 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                  DNA_BIND
DOMAIN
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DOMAIN
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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1D P53_PIG

1D P53_PIG

1D P7 16-1

DT 16-1

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DOMAIN
DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
  between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSOETFSDLWKLLPE----------NALLSSELSLAAVNDLLLSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VINWLDENPDDASRVPAP-----PAATAPAPAAPAPATSWPL--SSFVPSQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 YEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACPG
 Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                    DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 TYEMLLKIKESLELMQYLPQHTIETYRQ--QQQQQHQHLLQKQTSIQSPSSY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                       54;
                                                                                                                                                                                                                                                                    PROSITE; FSUUJAN, ...,
Anti-oncogene; DNA-binding; Transcription reyarrange.
Nuclear protein; Phosphorylation; Apoptosis.
Af TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                    BASIC (REPRESSION OF DNA-BINDING)
           FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                28.0%; Score 771; DB 1; Length 386; 40.3%; Pred. No. 8.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Mismatches 124; Indels
                                SUBUNIT: Binds DNA as a homotetramer (By similarity). SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                          A4C3D88E8DF55162 CRC64;
                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
OLIGOMERIZATION.
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                                                                                       SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                 EMBL; AF098067; AAF04620.1; -. HSSP; P04637; 1C26.
                                                                                                                                                                                                                                Pfam; PF00870; P53; 1.
PRINKTS: PR00386; P53SUPPRESSR.
Probom; PD002681; P53; 2.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                           42862 MW;
                                                                            many types of cancer.
                                                                                                                                                                                                                       InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                     166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                              285
349
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                           386 AA;
                                                                                                                                                                                                                                                                                                                          318
361
304
                                                                                                                                                                                                                                                                                                                                                                                385
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
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ID P53_F
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SOURCE STATE THE TELEFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Just. Med. Sci. 55:801-805(1993).

J. Vet. Med. Sci. 55:801-805(1993).

-1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
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PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
ک
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBGNIT: Binds DNA as a homotetramer (By similarity).
-:- SUBCELLULAR LOCATION: Nuclear.
-:- DISMARE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.
-:- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                               Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y., Watari T., Goitsuka R., Tsujimoto H., Hasegawa A.; "Cloning of feline p53 tumor-suppressor gene and its aberration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T., Goitsuka O'Brien S.J., Tsujimoto H., Hasegawa A.; "Molecular cloning and chromosomal mapping of feline p53 tumor suppressor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DO8B43BA1BC8EB78 CRC64;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R (IN REF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94114699; PubMed=8286534;
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Lymph node;
MEDLINE=94333960; PubMed=8056458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hematopoietic tumors.";
Int. J. Cancer 58:602-607(1994).
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 34-354 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42692
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Pfam; PF00870; P53; 1.
                                                                                                                                                                                           Felis silvestris catus
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386 AA;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9685;
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                                                                                                                                                            IP53 OR TRP53
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Length 386;

DB 1;

Score 770;

28.0%;

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NCBI_TaxID=9615;
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                                                                                                                                                DOMAIN
DNA_BIND
DOMAIN
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Best Local
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce).
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                                                                                  71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAI---- 126
                                                                                                                                                GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIIVTLETRDGQVLGRRCFE 302
                                                                                                                                                                                                                                                                                  303 ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELL 362
                                                                                                                                    ----PSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ 182
                                                                                                                                                                                   GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT 242
                                                                                                                                                                                                                                               205 FRHSVVVPXEPPEVGSDCTTIHYNFWCNSSCMGGWNRRPIITILILEDSNGKLLGRNSFE 264
                                                                                                                                                                                                                                                                                                   48
                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BCI-2
                                  LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                    14 LSQETFSELWILLPE------NNVLSSELSSAMNELPLSED---------
                                                                                                          -----VANWLDEA------PDDASGMSAVPAPAAPAPAT-----PAPAISWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
              60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of a cDNA encoding the chicken p53 nuclear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Tumor suppressor p53)
ed. No. 9.7e-45;
Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-1989 (Rel. 10, Created)
01-WAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                 363 YLPVRGRETYEMLLKIKESLEL 384
 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-SPAFAS;
MEDLINE-89083584; PubMed-3060861;
           58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellular tumor antigen p53
al Similarity 42.19
161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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P10360;
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            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 GRDRKIEEENFRK-----RGGAGGVAKRAMSPPTEAPEPPK-KRVLNPDNEIFYLQVR 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 AVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 PYEPPQVGTEFTTVLYNEMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LSP-EVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LEPTEVFMDLWSMLPY---SMQQL-----PLPEDHSNWQELS----PLEPSDPPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                       BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
FC37D0FCDF919586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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MEDLINE=98178659; PubMed=9519881;
Veldhor N., Milner J.;
"Isolation of canine p53 cDNA and detailed characterization of the full length canine p53 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
Canis.
                                                                                                                                                                                                                 Transcription regulation; Activator;
                                                                                                                                                                                                                               Nuclear protein; Phosphorylation; Apoptosis.
DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 2.1e-44;
50; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
1 p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 764.5; DB 1;
Pred. No. 2.1e-44;
                                                                                                                                                                                                                                                                              BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA
send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRETYEMLLKIKESLELMQ 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P53_CANFA STANDARD; PR Q29537; Q9TV78; O1-NOV-1997 (Rel. 35, Created) 15-DEC-1998 (Rel. 37, Last sequent 28-FEB-2003 (Rel. 41, Last annot Cellular tumor antigen p53 (Tumo
                                                                                                                       Pram; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
Prodom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Tr.
                                                                                                                                                                                                                                                                                                                                                                                        40169 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.68;
                                    EMBL; X13057; CAA31456.1;
PIR; S02193; S02193.
HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 169; Conservative
                                                                                                                                                                                                                                                                                                339
364
306
366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              308
347
292
366
367 #
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Page 10

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189

87

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PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP 309
                                                                                                                                                                                                                                                                                   88 KTYPGTYGFRLGFLHSGTAKSVTWTYSPLLNKLFCQLAKTCPVQLWVSSPPPPNTCVRAM 147
                                                                                                                                                                                                                                                                                                                                                          GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETYEMLLKIKESLELMQYLP-----QHT--IETYRQQQQQHQHLLQKQTSIQS 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ATSAPTAPGP--APSWPL----SSSVPSP
                                                    130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                        PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;

"Isolation of cDNAs encoding the p53 tumor suppressor gene in the
"Isolation of cDNAs encoding the p53 tumor suppressor gene in the
Japanese Medaka (Oryzias latipes).";

Submitted (MAX-1997) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes regulated for this process. One of
the activated genes is an inhibitor of cyclin dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthydae; Oryzinae; Oryzins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Japanese medaka
hotspots in MNNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
SUBGNIT: Binds DNA as a honcetramer (By similarity).
SUBCELDULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P33_CMAIL
P79820; Q9PSU7; Q9PSU8;
P79820; Q9PSU7; Q9PSU8;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryzias latipes (Medaka fish) (Japanese ricefish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krause M.K., Rhodes L.D., van Beneden R.J.; "Cloning of the p53 tumor suppressor gene from (Oryzias latipés) and evaluation of mutational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANT THR-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97305153; PubMed-9161419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 189:101-106(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
     64 P----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Himedaka;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exposed fish."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TP53 OR P53
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                                                                                                                                                                                                                                                                                                                                                          310
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AC P53_ORYILA
DT P53_OR
DT 01-NO
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DE CELIU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
A., Tsujimoto H.;
                                                                                                                                                                                                                                                                                                                  Kraegel S.A., Pazzl, K.A., Madewell B.R.;

"Sequence analysis of canine p53 in the region of exons 3-8.";

"Sequence analysis of canine p53 in the region of exons 3-8.";

"Sequence analysis of canine p53 in the region of exons 3-8.";

"Sequence analysis of canine p53 in the region of exons 3-8.";

"Incomplete the sa a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSD-PMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBGNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide variety
of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                Aberrations of p53 tumor suppressor gene in various spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC (REPRESSION OF DNA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY SIMILARITY).
MEES -> MQEP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY PRPK) (BY SIMILARITY).
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                                                                                                                                                                                                    Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> P (IN REF. 2).
761A718FDC93DA59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR LOCALIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
OLIGOMERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE P53 FAMILY.
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                                                                                                                                                                                                                                                                                                   MEDLINE-95323915; PubMed-7600529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF060514; AAC16909.1; -. EMBL, AA020761; BAA78379.1; -. EMBL, S77819; AAB42022.1; -. HSSP; P04637; 1046.
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PRODOM; PD002681; PS3; 1.
PROSITE; PS00348; PS3; 1.
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  Oncogene 16:1077-1084(1998).
                                                                                                                                                                                                                                                   SEQUENCE OF 25-300 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    many types of cancer
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                                                                                                 Setoguchi A., Sakai T.,
Watari T., Hasagawa A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375
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                                               SEQUENCE FROM N.A.
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299
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                                                                      TISSUE-Spleen;
                                                                                                                                                                             tumors in the
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAMPVYKKA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 FQELWETVSYP--PLETLSLPTVNEPTGSW-----VATGDMFLLDQDLS-----:55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
OLIGOMERIZARION
BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPQYTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 ---GTFDDKI-------FDIP---IEPVPTNEVNPPPTTVPVTTDYPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine), and Bos indiaus (28bu).
Bos indiaus (28bu).
Eukaryola: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                      PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                          Nuclear protein; Phosphorjiation; Apoptosis; Polymorphism.
DOMAIN 1 48 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                       ISSING (IN REF. 1).
196868A66351BFF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P53_BOVIN STANDARD; PRT; 386 AA. Q29628; 01.NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                         27.1%; Score 746.5; DB 1
43.1%; Pred. No. 3.3e-43;
tive 54; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                 S -> T.
MISSING (IN REF.
 or send an email to license@isb-sib.ch)
                                                                                         HSSP; P04637, 1YCS.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00306; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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RERYEFLKKINDGLELLE 329
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                               EMBL; U57306; AAC60146.1; -.
EMBL; AF003949; AAD01195.1; -.
EMBL; AF003950; AAD01196.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     39753 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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350
295
351
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NCBI_TaxID=9913, 9915;
                                                                                                                                                                                                                                                                                                                                                                                                   352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 163; Conserv
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SEQUENCE FROM N.A.
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DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                               VARIANT
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P53_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 SPYAQPSSTFDALSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTEL
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                                                                                   [2]
SEQUENCE OF 13-386 FROM N.A.
SECUES-Bovine; STRAIN-HOLStein; TISSUE-Thymus;
MEDLINE-96401400; PubMed-8807776;
KOMOTH H., Ishlquro N., Horiuchi M., Shinagawa M., Aida Y.;
Predominant p33 mutations in enzocitc bovine leukemic cell lines.";
Vet. Immunol. Immunopathol: 52:53-63(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBUNIT: Binds DNA as a homotetramer (By similarity).
-:- SUBCELDULAR LOCATION: Nuclear.
-:- DISBASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; Activator;
               Dequiedt F., Kettmann R., Burny A., Willems L.; "Nucleotide sequence of the bovine P53 tumor-suppressor cDNA."; DNA Seq. 5:261-264(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear protein; Phosphorylation; Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.9%; Score 740; DB 1; Length 386; 45.8%; Pred. No. 1e-42; ive 57; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY PRPK) (BY
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--- SIMILARITY: BELONGS TO THE P53 FAMILY.
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222473F28C548F31 CRC64;
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OLIGOMERIZATION
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MEDLINE=95352829; PubMed=7626789;
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EMBL; D49825; BAA08629.1; -.
EMBL; U74486; AAB51214.1; -.
PIR; S51648; S51648.
HSSP; P04637; ITUP.
InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00870; P53; 1.
PRINTS, PR00386; P533UPRESSR.
ProDom; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43255 MW;
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380
386 AA;
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Matches 15
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RPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPF 339
                                                                                                                                                                                               RONTHGIOMTSIKKRRSP-DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQ 398
                                                                   APPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=9737696; PubMed=9233767;
Reitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.W.;
Partial characterization of the woodchuck tumor suppressor, p53, and its interaction with woodchuck hepatitis virus X antigen in hepatocarcinogenesis.";
Oncogene 15:327-336(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Account of the property of the physiological growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BCI-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear. DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                            16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                       399 QQQQQH-QHLLQKQTSIQSPSSYGNSSPPLNK 429
                                                                                                                                                                                                                                                                   353 GESRAHSSHLKSK----KRPSPSCHKKPMLKR 380
                                                                                                                                                                                                                                                                                                                                                    391 AA
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ProDom; PD002681; P53; 1.
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HSSP; P04637; 1TUP.
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PROSITE; PS00348; P53; 1.
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                                                                                                                                                                                                                                                                                                                                       14 LSQETFSDLWNLLP-----ENNVLSPVLSP 38
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                                                                                                                                                                                                                                                                                                      11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
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                                                                                                                                                                                                                                                                                                                                                                                                                   39 PMDDL-LLSSED--VENWFDK----GPDEALQMSAAPAPKAPTPAASTLAAPSPATSWPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 VRVCACPGRDRRTEEENFRKR------GEPCPEPPPRSTKRALPNGTSSSPQPKKKPL
                                                                                                       PHOSPHORYLATION (BY PRPK) (BY SIMILARITY).
                                                                                                                                                                                                                                                                  78; Gaps
Transcription regulation; Activator;
               Phosphorylation; Apoptosis.
44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                         BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                  PHOSPHORYLATION (BY SIMILARITY). E1DE5DB84BA40182 CRC64;
                                                                                                                                                                                                                            Length 391;
                                                                                                                                                                                                                                                                70; Mismatches 121; Indels
                                                                                                                                                                                                                            ; DB 1;
1.4e-42;
                                                   BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                            26.8%; Score 738; 37.7%; Pred. No. 1
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ne : 11.1507 secs
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DNA-binding;
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                                                   290
354
385
321
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                   Nuclear protein;
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323
366
309
15
Anti-oncogene;
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DNA_BIND
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SEQUENCE
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DOMAIN
DOMAIN
MOD_RES
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Q9plb6 homo sapien O91158 homo sapien O91592 homo sapien O99149 rattus norv Q9up74 homo sapien Q8162 brachydanio Q8162 brachydanio Q8162 brachydanio Q8162 mus musculu Q98sw0 xenopus lae Q9k64 barbus barb Q9152 mus musculu Q8151 mus musculu Q8155 homo sapien Q8cdy5 homo sapien Q8cdy6 homo sapien Q8cdy7 mus musculu Q8cdy6 homo sapien Q96x77 mus musculu Q8cdy6 homo sapien
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089097 mus musculu
099162 rattus norv
090132 homo sapien
099161 rattus norv
099160 rattus norv
088897 mus musculu
Ogubv9 homo sapien
Ogp1b4 homo sapien
O75080 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                     ALIGNMENTS
          09P1B4
075080
089097
099JE2
09DEC7
09H3D2
                                                                           099JE0
08897
09H3P8
075922
09JD9
09UP74
08JHZ5
08JHZ5
08JHZ9
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Q8TDY5
Q8C826
Q8TDY6
Q9CU77
                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                          PRELIMINARY;
  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                            09UP27
 09н3D3;
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                                                                                                                                                                                                                                                                                                                                RESULT 1
Q9H3D3
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                                                               August 7, 2003, 09:41:09; Search time 41.5172 Seconds (without alignments) 3207.225 Million cell updates/sec
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                                                                                                                          .......HCTPPPYPTDCSIVRIWQV 516
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2751
1 MSQSTQTNEFLSPEVFQHIW.
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DO 994303 PRELIMINARY; PRT; 555 AA.

AC 09H303; O9UP27;
DI 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-CCT-2002 (TrEMBLrel. 12, Last annotation update)
DE TA p63 beta.
GN HOMO sapiens (Human).
CN ENARYOCA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBL_TAXID-9606;
RN FILTAXID-9606;
RN YANGA A. Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., RA Andrews N.C., Caput D., McKeon F.;
RN Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.;
RN Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., R. MEDLINE-98448095; PubMed-9774969;
RR Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., R. Mallawara K., McKeon F.;
RN Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., R. Mol. Cell 2:305-316(1999).
RN SEQUENCE FROM N.A.
RA Hagiwara K., McKenenmin M.G., Harris C.C.;
RL SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -: SUBLIARITY: BELONGS TO THE P33 FAMILY.
DR BMBL; AF124539; AAG45608.1; JOINED.
DR EMBL; AF124539; AAG45608.1; JOINED.
DR EMBL; AF124534; AAG45608.1; JOINED.
DR EMBL; AF124554; AAG45608.1; JOINED.
DR EMBL; AF124554; AAG45608.1; JOINED.
DR EMBL; A

09h3d3 homo sapien 09plb7 homo sapien 075195 homo sapien 09h3d4 homo sapien 099jd7 rattus norv 099jd8 rattus norv 099jd8 rattus norv 099jd8 rattus norv 09jp6 rattus norv 09jp6 rattus norv 08h898 mus musculu

0,09H3D3 0,09F1B7 0,09H3D4 0,99JD7 0,99JD8 0,90JB1 0,90JF8 0,90JF8 0,09B89 0,09B89 0,09B89 0,09B89 0,09B89 0,09B89 0,09B89 0,09B89

99.7 998.7 998.7 998.7 998.7 998.7 998.7 998.7 998.7 997.6 997.6 997.6 985.5 985.5

2751 2744 2722 2722 2714 2714

2714 2714 2685 2685 2685 2449 2372 2372 2352

Description

Query Match Length DB

Result No. homo sapien homo sapien homo sapien 9 mus musculu

Q9nph7 hc Q9up26 hc Q9p1b5 hc Q9qwy9 n ~

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AAF43488.1; J
                                                                          AF116767; AAF43488.1;
                                                                                                                      ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                               Best Local Similarity 99.8
Matches 515; Conservative
                                                                                             InterPro; IPR002117; P53
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                                                                                                      Pfam; PF00870; P53; 1
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SEQUENCE FROM N.A.
                           AF116762;
AF116763;
AF116764;
AF116765;
AF116766;
         AF116760;
AF116761;
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SEQUENCE 516
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
P51 isoform Tap63beta.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; ARI10769; AAR434881; ...
EMBL; AR116755; AAR434881; JOINED.
EMBL; AR116755; AAR434881; JOINED.
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                                                                          DB 4; Length 555;
                                                                                             Indels
                                                       E22874BE7DBABCBE CRC64;
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Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto
Yokota J.;
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100.0%; Pred. No. 2e-223;
11ve 0; Mismatches 0;
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     Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                             Nuclear protein.
SEQUENCE 555 AA; 62433 MW;
InterPro; IPR002117; P53.
                                                                                 Best Local Similarity 100.
Matches 516; Conservative
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                                                                         Query Match
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last annotation update)
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                                                                                                                                                                                                                                                                                  99.7%; Score 2744; DB 4; 99.8%; Pred. No. 7.2e-223;
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01-NOV-1998 (TrEMBLrel. 08, Last sequen
01-OCT-2002 (TrEMBLrel. 22, Last annota
P51 isoform TAP63ALPHA (P51B protein)
Homo sapiens (Human).
JOINED.
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JOINED.
JOINED.
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421 GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
Lransactivating, deach-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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A Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
REBL; AF124539; AAG45607.1; JOINED.
REBL; AF124539; AAG45607.1; JOINED.
REBL; AF124531; AAG45607.1; JOINED.
REBL; AF124533; AAG45607.1; JOINED.
REBL; AF124533; AAG45607.1; JOINED.
REBL; AF124535; AAG45607.1; JOINED.
REBL; AF124535; AAG45607.1; JOINED.
REBL; AF124535; AAG45607.1; JOINED.
REBL; AF124535; AAG45607.1; JOINED.
REBL; AF124536; AAG45607.1; JOINED.
REBL; AF124536; AAG45607.1; JOINED.
REBL; AF124536; AAG45607.1; JOINED.
REBL; AF124538; AAG45607.1; JOINED.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              680 AA; 76785 MW; F66ECD45E87D9799 CRC64;
                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
TA p63 alpha (Tumor protein p63).
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100.0%; Pred. No. 7.5e-221;
ive 0; Mismatches 0;
                                                           481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511
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                                                                                                                                                               PRELIMINARY;
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Matches 511
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         MEDLINE-98324755; Pubbwed-9662378; Osada M., Obba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I., Ikawa Y., Nimura Y., Nakagawara A., Obinata M.; "Cloning and functional analysis of human p51, which structurally a functionally resembles p53."; Nat. Med. 4:839-844(1998).
                                                                                                                                                            Yokota J.; "Mutation and expression of the p51 gene in human lung cancer."; Neoplasia 1:71-79(1999).
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                                                                                                                                             Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa
Yokota J.;
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-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AB016073; BAA32593.1; -.
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SEQUENCE FROM N.A.
MEDLINE-20388515; PubMed=10935472;
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ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
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Interpro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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Matches 511; Conservative
TISSUE-Skeletal muscle;
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SEQUENCE 641 A
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GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL 480
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                                                                                                                                                                                        DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                          SPSPAIPSNIDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                            203 PQGAVIRAMPVXKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                 301 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
MSQSTQTSEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSENGATNKIEISMDCIRMQ
                              PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                      241 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHULLQKQTSIQSPSSY
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PRINTS; PR00386; P53SUPPRESSR.
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98.4%;
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Best Local Similarity 98.4'
Matches 508; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE 555 A
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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Last annotation update)
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Pred. No. 2.6e-220;
5; Mismatches 3;
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MEDLINE=21363378; PubMed=11470269;
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98.4%;
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                Last sequence update)
Last annotation update)
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FEBS Lett. 501:121-126(2001).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AJ277451; CAG37103.1; -.
HSSP; P04637; 1YCS.
InterPro; IRR002117; P53.
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Pred. No. 2.7e-220;
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5; Mismatches
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TISSUE-skeletal muscle, and Keratinocytes;
MEDLINE-99018225; PubMed-9799841;
Augustin M., Bamberger C., Paul D., Schmale H.;
"Cloning and chromosomal mapping of the human p53-related KET gene to chromosome 3q27 and its murine homolog Ket to mouse chromosome 16.";
Mamm. Genome 9:899-902(1998).
                                                                                                                                                                             DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                              SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPP
                                                                                                                                        SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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                         40 MSQSTQTSEFLSPEVFQHIMDFLEQPICSVQPIELNFVDEPSENGATNKIEISMDCIRMQ
                                                                                                                                                               PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last annotation update)
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; Y16901; CAA76562.1; -.
HSSP; P04637; LYCS.
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ProDom; PD002681; P53; 1.
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InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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PROSITE; PS00348; P53; 1
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DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.
Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998)
--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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Last sequence update)
Last annotation update)
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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HSSP; P04637; 1YCS.
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InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
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Matches 508; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE 555
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                                                                                      1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
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                                      Length
                                                               Indels
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-!- SUBCELLULAR LOCATION: NUCLERR (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL: Y10258; CAB88216.1; -.
HSSP; P04637; 1XCS.
             C953BBAC389D5B70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                      Score 2685; DB 11;
Pred. No. 9.6e-218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511
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MEDLINE-97460723; PubMed=9315105;
Schmale H., Bamberger C.;
"A novel protein with strong homo
             74660 MW;
                                   97.6%;
illarity 98.4%;
Conservative 5
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              663 AA;
                                                  Similarity
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Best Local Simi
Matches 503;
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                                                1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDILIDE-2136378; PubMed=11470269;
Bamberger C., Schmale H.;
"Identification and tissue distribution of novel KET/p63 splice
                          ö
Length 680;
                          Indels
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Last sequence update)
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Score 2714; DB 4;
Pred. No. 3.6e-220;
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98.78;
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             Similarity
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THE P53 FAMILY
                            MGD; MGI:1330810; Trp63.
InterPro; IPR00117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                      680 AA; 76788 MW;
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Eukaryota; Merazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
  -!- SIMILARITY: BELONGS TO T
EMBL; AF075436; AAC62641.1;
HSSP; P04637; 1YCS.
                                                                                                   PROSITE; PS00348; P53; 1
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MEDLINE=98448095; PubMed=9774969;
Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
Caput D., McKeon F.;
"p63, a p53 homolog at 3427-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                        1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                   PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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Murinae; Mus
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                                                                                                   DB 11; Length 680;
                                                                                                                     Indels
                                                                                AC45DABB88F61400 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
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Last annotation update)
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                Score 2685; DB 11;
Pred. No. 1e-217;
5; Mismatches 3;
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InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; I.
PRINTS; PR00186; P533UPPRESSR.
ProDom; PD002081; P53; I.
SMART; SM00454; SAM; I.
                                                                              680 AA; 76760 MW;
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                                                          PROSITE; PS00348; P53; 1.
Nuclear protein.
                                                                                               Query Match
Best Local Similarity 98.4
Matches 503; Conservative
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                                                                                                        1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=20388515; PubMed=10935472; MEDLINE=20388515; PubMed=10935472; Panil M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S., Yokota J.; "Mutation and expression of the p51 gene in human lung cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                  680;
                                  DB 11; Length
                                                                    Indels
8DFF0284F247C68A CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
P51 isoform TApG3delta (P51 delta protein).
                              / Match 97.6%; Score 2685; DB 11;
Local Similarity 98.4%; Pred. No. 1e-217;
hes 503; Conservative 6; Mismatches 2;
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70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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                     SEQUENCE FROM N.A.
MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3427-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.5%; Score 2379; DB 4; Length 461; 100.0%; Pred. No. 3.7e-192; ive 0; Mismatches 0; Indels
                                                                                                                                             Hagiware K.) McMenamin M.G., Harris C.C.;
Hagiware K., McMenamin M.G., Harris C.C.;
Submitted (JAN-1999) to the EMBL/Genbank/DDBJ databases.
-!- SUBCELLULAR LOCATION: UNCLEAR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: UNCLEAR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: UNCLEAR (BY SIMILARITY).
-!- SUBCELLULAR TO THE P53 FAMILY.
REMBL; AR724533; AAG45611.1; -- INTED.
REMBL; AF124531; AAG45611.1; JOINED.
REMBL; AF124532; AAG45611.1; JOINED.
REMBL; AF124534; AAG45611.1; JOINED.
REMBL; AF124535; AAG45611.1; JOINED.
REMBL; AF124535; AAG45611.1; JOINED.
REMBL; AF124535; AAG45611.1; JOINED.
REMBL; AF124537; AAG45611.1; JOINED.
REMBL; AF124537; AAG45611.1; JOINED.
REMBL; AF124537; AAG45611.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                     461 AA; 51404 MW; 68B63547A46C1B05 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 447; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 461 AA; 51404
                                                                                                                                                                                                                                                                                                                                          P04637; 1YCS.
                                                                                                                                    SEQUENCE FROM N.A.
NCBI_TaxID=9606;
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Q9P1B5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                           Length 471;
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                                                                                                                                                                                                                                                                                                471 AA; 52882 MW; 32EB39798FC1CE69 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                         Score 2449; DB 4; I
                                                                                                                                                                                                                                                                                                                                  100.0%; Prec. ...
           -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIM:
L-! SIMILARITY: BELONGS TO THE P53 FAMILY
EMBL; AFI16771; AAF61624.1; --
EMBL; AFI16769; AAF43489.1; --
                                                 Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22, DN P63 beta.
                                                                                                                                                                                                                                                                                                                           89.08;
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InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                        ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
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Matches 463; Conservative
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Neoplasia 1:71-79(1999)
                                                                                                                                                                                                                                                                                    Nuclear protein.
SEQUENCE 471 P
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                                                                                                                                                                                                                                                                                                                            Query Match
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ID Q9UP26
AC Q9UP26;
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                                                                     P51 isoform delNbeta.
Momo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                              "Mutation and expression of the p51 gene in human lung cancer."; Neoplasia 1:71-79(1999).

--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

--- SIMILARITY: BELONGS TO THE P53 FAMILY.

EMBL; AF116769; AAF43492.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-20388515; Pubmed-10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2372; DB 4; Length 461;
Pred. No. 1.5e-191;
0; Mismatches 1; Indels (
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                           Created)
Last sequence update)
Last annotation update)
 461 AA
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                                                                                                                                                                                                                                                                                 EMEL, AF116758; ARF43492.1; JOINED. EMEL, AF116759; ARF43492.1; JOINED. EMEL, AF116761; ARF43492.1; JOINED. EMEL, AF116761; ARF43492.1; JOINED. EMEL, AF116762; ARF43492.1; JOINED. EMEL, AF116764; ARF43492.1; JOINED. EMEL, AF116765; AAF43492.1; JOINED. EMEL, AF116765; AAF43492.1; JOINED. EMEL, AF116767; AAF43492.1; JOINED. HSSP; P04637; LYCS.
 PRT;
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PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PNCSTTE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 461 AA; 51305 MW; 6
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                         01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2002 (TrEMBLrel. 22,
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 PRELIMINARY;
                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
                                                                                                                                                                                                                MEDLINE=9848095; PubMed=9774969;
MEDLINE=9848095; PubMed=9774969;
Vang A., Kaphad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
-! SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
-! SINILARITY: BELONGS TO THE P53 FAMILY.
EMBL, AF075438; AAC62643.1;
-- HSSP; P04637; 1YCS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                      (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.6%: Score 2356; DB 11;
98.9%; Pred. No. 3.2e-190;
tive 3; Mismatches 2;
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435 LSMPSTSHCTPPPPYPTDCSIVGIWOV 461
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ProDom; PD002681; P53; 1.
PROSITE; P800348; P53; 1.
SEQUENCE 461 AA; 51455 MW:
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InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
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                                                               PRELIMINARY;
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01-OCT-2002
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Search completed: August 7, 2003, 09:51:38 Job time : 42.5172 secs

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August 7, 2003, 09:31:28; Search time 30.8966 Seconds (without alignments) 2301.535 Million cell updates/sec
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1 MSGSTQTNEFLSPEVFQHIW.....PKQSDVFFRHSKPPNRSVYP 448
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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/SIDS1/gcgdata/geneseqyemeseqp-emb1/AA1983.DAT:
/SIDS1/gcgdata/geneseqyemb1/AA1984.DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Human pol protein	Human cell requlat	Human p63 protein	Human protein #1 u	Human oncodene p51	Human oncodene p51	Human oncodene p63	Human lung cancer	Human p53 homologu
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SUMMARIES			ID		AAY45246	AAY05955	AAB11359	AAB82128	ABG95127	ABG95137	ABG95143	ABP61911	ABB74991
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			e Match Length DB]		448	448	448	448	448	448	448	448	448
	æ	Query	Match	1 0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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ABUS6418 AANS05961 AARS055129 ABG95129 AARB1363 AARB11363 ABG95141 AARB1361 AARS0998 AARS0998 AARS0998 AARS0997 AARS0998 AARS0998 AARS0998 AARS0998 AARS0998 AARS0998 AARS0998 AARS099130 AARS095130 AARS095130 AARS095130 AARS055130	Lung cancer-associ		oncodene	regu	Human p63 protein	gene	jene	Human lung cancer		Human p51 protein		Human p63 protein		Human oncogene p5B			Human lung cancer		Human p63 protein		Human lung cancer	Human p53 homologu	Human cell regulat	Rat KET protein.	Human cell regulat	Human oncogene p51	Human oncogene p63		Human oncogene p51	. Human p63 protein	Human oncogene p51	Jene		_	Human cell regulat
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	AAY45246 standard; Protein; 448 AA.				st entry)		Α.		Human: p51: p53 related gene: cell proliferation: regulat
	standard; Pr				07-JAN-2000 (first entry)	•	Human p51 protein A.		1: p53 relat
RESULT 1 AAY45246	AAY45246		AAY45246;		07-JAN-20		Human p51		Human: p5
RES!	Ω	X	AC	X	DŢ	×	DΕ	XX	3

ALIGNMENTS

tion; cancer; 1..59 /label= transactivation_domain 142..31 /label= DNA_binding_domain 353..397 Location/Qualifiers tumour suppression; diagnosis. Homo sapiens Key Domain Domain

353..397 /label= oligomerisation_domain 99WO-JP01512. 98JP-0100467 W09950412-A1 24-MAR-1999; 27-MAR-1998; 07-OCT-1999. Domain

(SAKA) OTSUKA PHARM CO LTD.

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Homo sapiens.
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                                                                                                                                                                                                                                                                         The present sequence represents a human p51 protein, which is related to p53 and has cell proliferation requiation and tumour suppression activity. The p51 gene can be used in the investigation, diagnosis and treatment of diseases such as cancer, with which the p53 family cell proliferation regulation is associated. The p51 protein may be used for screening potential agonists and antagonists of its regulatory function, for use as drugs,
                                                                  investigation and proliferation
                                                                                                                                                                                                                                                                                                                                                    1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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                                                                                                                                                                                                                            Length 448;
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                                                                  New p53 related human gene p51, useful for diagnosis, treatment of cancers and screening for potential cell
                                                                                                                                                                                                                        Query Match 100.0%; Score 2383; DB 20; Best Local Similarity 100.0%; Pred. No. 4.7e-207; Matches 448; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 147-148; 163pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY05955 standard; Protein; 448 AA.
                    Obinata M;
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                                      WPI; 1999-591318/50
                    Ikawa S,
                                                                                                                                                                                                       448 AA;
                                                N-PSDB; AAZ25770
(IKAW/) IKAWA Y.
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                    Ikawa Y,
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The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position intron. The human p53 gene was localised to chromosomal position intron. The human p53 gene was localised to chromosomal position intron. The human p53 gene was localised to chromosomal position gamma forms, while p63 members differing in the Nterminus are designated as deltaN and TA forms, where the deltaN form lacks the cransactivation domain. The present sequence represents human p63 sequence rissue. It demonstrates remarkably divergent b63 isotype TAp63 gamma. P63 was detected in a variety of many play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. Cachexia) and neuronal differentiation and related degenerative disorders. p63 may also be implicated in haematopolesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative AXX58722-83) and anti-p63 antibodies of the invention can be used to the dentify compounds useful for treating disorders involving such transgenic animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated p63 cell regulatory protein for, e.g. treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23; Fig 11; 161pp; English.
                                                                     98US-0087216.
98WO-US21992
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Matches 448; Conservative
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                                                                                                                                                                                                                                                                                                                                 WPI; 1999-277595/23
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02-OCT-1998;
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                                                                                                                                     SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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    Length
                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytostatic; gene therapy; p53; human tumour.
Score 2383; DB 21;
Pred. No. 4.7e-207;
Mismatches 0;
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/label= DNA_binding_domain
353..397
/label= Oligomerisation_domain
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                              448; Conservative
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N-PSDB; AAF86588.
                  Similarity
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   Ouery Match
Best Local S
Matches 448
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AAB82128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC 300 HIHIHIHIHIHIHIHIHIHIHIH 300 241 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC 300
                                                                                        360
                                                                                                    comprising an immunogenic portion of a lung funct protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccinas to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention and be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient cells expressing P2 and then administered to the patient to inhibit
 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
                                                                                                                                               LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient -
                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
                                                                                       FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel isolated polypeptide (I) which
                                                                                                                                                                                                                         LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 247-249; 261pp; English.
                                                                                                                                                                                                                                                                                                           AAB11359 standard; Protein; 448 AA
                                                                                                                                                                                                                                                                                                                                                                                                   Human p63 protein isoform #3
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99US-0476496.
2000US-0480884.
2000US-0510376.
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N-PSDB; AAC66029.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; detection
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30-DEC-1999;
10-JAN-2000;
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                                                                                The present invention relates to a chimera gene of p53 family encoding a transcription activating region, a DNA binding region, and an oligomer formation region of different p53 family proteins. The chimeric gene can be used for gene therapy of p53 variant human tumours, and analysis of the function of the p53 family gene. The present sequence was used in the
                                                                                                                                                                                                                                                                                                                                                                                                    ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC 300
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Chimera gene of the p53 family, useful for gene therapy, and treatment of cancer, comprises a transcription activating region and a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein 90;
                                                                                                                                                                                                                                                                                   DSDLSDPMWPQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                                                                                                                                                                                                                                                    SPSPAIPSNIDYPGPHSFDVSFQQSSTAKSATWIYSTELKKLYCQIAKTCPIQIKVMIPP
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                                                                                                                                                                                                                                                                     1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferative disease; cellular protein isoform; heat shock protein HSP-90; rheumatoid arthritis; cancer; haematopoletic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML; acute lymphoblastic leukaemia; ALL; APU; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
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                                                                                                                                                                                                                 Length 448;
                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                               100.0%; Score 2383; DB 22; 100.0%; Pred. No. 4.7e-207;
                                                                                                                                                                                                                                          Mismatches
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                                                      Example 1; Page 30-32; 57pp; Japanese
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                                                                                                                                                                                    448 AA;
                             binding region
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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating proliferative diseases associated with mutant cell population, treating proliferative diseases associated with mutant cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein or cellular protein isoforms (II) dependent on heat shock involving administering HSP90 inhibitor. The method is useful for involving administering HSP90 inhibitor. The method is useful for creating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cells concaining fusion protein in heterogeneous call population, treating proliferative disease (e.g. rheumatoid arthritisty cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein or cellular protein isoform dependent on heat shock protein or cellular protein in a patient heterozygous for (II). The method is useful protein isoform in a patient heterozygous for (II). The method is useful (in treating a disease e.g. hemantopoletic disorder such as T or B cell in Importation or chronic myeloid leukaemia (CML), APL, AML, MML and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
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                                                                                                                                                                                                                                                                                               Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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100.0%; Pred. No. 4.7e-207;
ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 320-321; 389pp; English.
                                                                                                                                                        (CONF-) CONFORMA THERAPEUTICS CORP
                                                                            01-MAR-2002; 2002WO-US06518
                                                                                                                   01-MAR-2001; 2001US-272751P
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Best Local Similarity 100.
Matches 448; Conservative
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WO200269900-A2.
                                       12-SEP-2002
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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (1), treating cancerous cells containing (1) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (11) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (11) in administering HSPD-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion concogenic fusion protein, treating cancerous cells containing fusion or cancer) associated with mutant protein or cellular protein la patient heterographs for (11). The method is useful for treating a disease e.g. heematopoietic disorder such as T or B cell (15) treating a disease e.g. heematopoietic disorder such as T or B cell (17) managed the containing the containing the containing the containing the containing containing the containing containing the containing disease e.g. heematopoietic disorder such as T or B cell (17) managed the containing the 
                                LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein griffs+90; rheumatoid arthritis; cancer; haematopoietic disorder; real lymphona; B cell lymphona; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML; acute lymphoblastic leukaemia; ALL; APL; NLI; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                                                                                       421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
                                                                                                             LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
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                                                             1 MSQSTQTNEFLESPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIELSMDCIRMQ
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                                               1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMO
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                          Gaps
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             4.7e-207
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100.0%; Score 2383;
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448; Conserv
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N-PSDB; ABS73335.

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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (MSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for [II]. The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid excitoma, bwing's sarrooma, melanoma, liposarrooma, rhabdomyosarrooma and synovial sarrooma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
                     Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                              Disclosure; Page 354-356; 389pp; English
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                                      DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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       100.0%; Score 2383; DB 23;
100.0%; Pred. No. 4.7e-207;
ive 0; Mismatches 0; 1
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ABP61911 standard; Protein; 448 AA.

RESULT 8 ABP6191 ABP61911;

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polynucleotides (1) and polypeptides (11) and (11) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (1) or (11) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (1) can be used for detecting the presence of a cancer in a patient, by obtaining a bloiogical sample from the patient, contacting the sample in the patient, contacting the biological sample with the Oligonucleotide, detecting in the sample, amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide and compositions, e.g. vaccines. (I) are useful in paramaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer.

ARQ02145 to ARQ02486 and ABR01866 to ABR01922 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                   Vedvick TS;
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                                                                                   Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine
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                                                                                                                                                                                                                                                                                                                                                                      Henderson RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes isolated human lung carcinoma
                                                 Human lung cancer associated protein sequence SEQ ID NO:340.
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Durham M, Fanger GR,
W, Cai F, Foy TM;
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100.0%; Pred. No. 4.7e-207;
iive 0; Mismatches 0;
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Retter MW, Dv
Peckham DW, (
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McNeill PD, Fanger N, Retter
Carter D, Watanabe Y, Peckha
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07-MAY-2001; 2001US-0850716.
28-JUN-2001; 2001US-0897778.
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              (first entry)
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Matches 448; Conservative
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                                    MSOSTOTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMO
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             Indels
  No. 4.7e-207;
              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer-associated polypeptide #11.
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2001US-290492P.
2001US-339245P.
2001US-350666P.
 100.08;
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             448; Conservative
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N-PSDB; ABX76134.
  Best Local Similarity
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10-MAY-2001; 2
09-NOV-2001; 2
13-NOV-2001; 2
29-NOV-2001; 2
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              ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC 300
                                               FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360
                                                                                           LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes human lung tumour proteins. Human lung tumour proteins and polynuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynuclectides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABI48959 to ABI49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                    Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -
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                                                                                                                                                                                                                                                                                           Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henderson
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McNeill PD, Fanger N, Retter MW, Marnerakis M,
Vedvick TS, Carter D, Watanabe Y, Peckham DW;
                                                                                                                                       Score 2383;
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2000US-0685696.
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2001US-0850716.
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2000US-0643597,
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09-OCT-2000;
12-DEC-2000;
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21-AUG-2000;
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McNeill
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16-AUG-1999 (first entry)

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynuclectide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynuclectides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methods are useful for treating undersory compound usuallised line methods are useful for treating lung cancer, such as small cell lung cancer or other benign or precancerous cancer, non-small cell lung cancer or other benign or precancerous persons is, e.g. arbectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56408-ABU56745 represent lung cancer, such as polypeptides of the invention.
                             Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
                                                                                                                                                                                      Claim 27; Page 196; 453pp; English.
                                                                                                                              expression in lung cancer
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448 AA; Sequence

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                                                  1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGAINKIEISMDCIRMQ
                                       1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                                                ITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                        PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                     Gaps
100.0%; Score 2383; DB 24; Length 448; 100.0%; Pred. No. 4.7e-207; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                  LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
                                                                                                                                                                                                                                                                                                                             448; Conservative
         Local Similarity
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The present invention concerns the discovery of a new family of cell regulatory proteins (CRPS) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using capped corner and proteins p53 and p73. Mouse p63 cDNA was isolated using capped corner and the mapilified cDNA possessed a truncated N-terminus. i.e. the amplified cDNA possessed a truncated N-terminus. i.e. the capped corner and the corner protein a probe corresponding to exons 5-9 of p63. At least 6 different isotypes exist. Splice to exons 5-9 of p63. At least 6 different isotypes exist. Splice variants differing at DNA intrary with a probe corresponding corner and gamma forms, while p63 mesers designated as deltaN and TA forms, where the deltaN form lacks the transactivation domain. The present sequence represents mutine p53 isotype muTAp63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression and induce apoptosis. Cessation or down-regulation of p63 expression act as dominant hegatives towards transactivation by p53 and p63. CC achexia) and neuronal differentiation and related degenerative disorders p63 may also be implicated in heematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAX58512-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated p63 cell regulatory protein for, e.g. treatment of
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                                                                                Cell regulatory protein; p63; muTAp63 gamma; TAp63 gamma;
                                                                                                         cancer; tumour suppressor; cell cycle control; apoptosis;
cell proliferation; cell differentiation; therapy.
                                          Mouse cell regulatory protein p63, isoform muTAp63 gamma
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97US-0062076.
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Best Local Similarity 96.9
Matches 434; Conservative
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N-PSDB; AAX58580.
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15-OCT-1997;
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AAY05961 standard; Protein; 483 AA.

RESULT 11 **AA**Y05961 AAY05961;

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SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proteins diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 90; HSP-90; rheumatoid arthritis; cancer; heamatopoietic disorder; cell lymphona; Beell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; ALL; ALL; NLL; solid tumour; chronic myeloid sactiona; should carcinoma; bying's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
                SPSPAIPSNIDYPGPHSFDVSFQQSSTAKSATWIYSTELKKLYCQIAKTCPIQIKVMTPP
                                                       PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                      ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                            FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                      LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQHQHLLQKHLLSACFRNE
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                                                                                                                                                                                                                                                                                                     Disclosure; Page 325-327; 389pp; English.
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N-PSDB; ABS73329.
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Through administrating most-yu-imministron is measured as better the introduced administrating most-yu-imministron yielding oncogenic fusion protein, treating cancerous cells containing fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. heematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
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protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosome aberration; oncogenic fusion protein; cancer; oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2185; DB 23;
Pred. No. 4.4e-189;
3; Mismatches 7;
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94.1%;
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                                                                                                                                                                                                                                                                                                    The invention describes a method of treating genetically-defined disease associated with chromosomal abbrrations yielding oncogenic fusion proteins (1), treating cancerous cells containing (1) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein or cellular protein isoforms (II) dependent on heat shock protein or selectively treating cells expressing (II) involving administering HSSD-140, treating centerous cells expressing (II) involving administering disease with chromosomal aberration yielding protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or protein isoform dependent on heat shock protein (HSP)-90 (e.g. protein isoform isoform dependent on heat shock protein or cellular protein a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukemia (CML), APL, AML, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, libosarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSDLSDPMWPQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
                                                                                                                                                                                                                 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.7%; Score 2185; DB 23; Length 471; 94.1%; Pred. No. 4.4e-189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                               Disclosure; Page 335-336; 389pp; English.
                                                                                                                                       CONF-) CONFORMA THERAPEUTICS CORP.
                                                                                    01-MAR-2002; 2002WO-US06518.
                                                                                                              01-MAR-2001; 2001US-272751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 94.1 Matches 416; Conservative
                                                                                                                                                                 Burrows FJ;
                                                                                                                                                                                        WPI; 2002-698710/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 AA;
                                  WO200269900-A2.
            Homo sapiens.
                                                            12-SEP-2002.
                                                                                                                                                                 Fritz LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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301 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360

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                                                                           LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE 420
301 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell regulatory protein; p63; huTAp63 beta; TAp63 beta; human;
                                                                                                                      cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cell regulatory protein p63, isoform huTAp63 beta.
                                                                                                                                                                                                                                            421 LVEPRRETPKQSDVFFRHSKPP 442
                                                                                                                                                                                                                                                                                                                       ----QTSIQSPSSYGNSSPP 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY05954 standard; Protein; 516 AA
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97US-0062076.
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15-0CT-1997;
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                                                                                                                                                                                                                                                                                                                                                                           cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
                                                                    1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                             SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                                                      PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                                                 ITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                         LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQHQHLLQKHLLSACFRNE
                                                                                                                                                                                                                                                Gaps
identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.
                                                       16;
                                         Length 516;
                                                       Indels
                                         91.7%; Score 2185; DB 20;
94.1%; Pred. No. 5.1e-189;
ive 3; Mismatches 7;
                                                                                                                                                                                                                                                                            LVEPRRETPKQSDVFFRHSKPP 442
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99US-0466396.
99US-0476496.
2000US-0480884.
                                                                                                                                                                                                                                                                                                                                                             Human p63 protein isoform #7
                                                                                                                                                                                                                                                                                                                    AAB11363 standard; Protein;
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                                               Best Local Similarity 94.1
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17-DEC-1999;
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                                                                                                                                                                                                                               comprising an immunogenic portion of a lung timer protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
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                                                                    Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient \cdot
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Pred. No. 5.1e-189;
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                                                                                                                                                               Disclosure; Page 255-256; 261pp; English
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94.18;
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WPI; 2000-628399/60.
N-PSDB; AAC66033.
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Job time: 31.8966 secs
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7, 2003, 09:42:54; Search time 12.3586 Seconds (without alignments) 1533.769 Million cell updates/sec
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1 MSQSTQTNEFLSPEVFQHIW......PKQSDVFFRHSKPPNRSVYP 448
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

3, App 3, App 3, App 1, App Appli Sequence 340, 152, 152, 152, Description sednence sed Sequence US-09-643-597-152 US-09-480-884A-152 US-09-542-615A-152 US-09-606-421B-152 US-09-542-615A-344 US-09-606-421B-344 US-09-643-597-339 US-09-606-421B-339 US-09-643-597-342 US-09-542-615A-342 US-09-606-421B-342 US-09-542-615A-339 -09-542-615A-343 US-09-606-421B-343 US-09-643-597-341 .09-542-615A-341 -09-277-196-19 SUMMARIES DB Length Query Match 1 100.0 100.0 100.0 91.7 901.7 901.7 901.7 901.7 901.7 901.7 Score Result No.

241 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC 300

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Seguence

Sequence 20, Appl Sequence 3, Appl Sequence 27, Appl Sequence 27, Appl Sequence 8, Appl Sequence 8, Appl Sequence 2, Appl Sequence 17, Appl Sequence 25, Appl Sequence 26, Appl Sequence 2, Appl Sequence 3, Appl Sequence 32, Appl Appl Sequence 32, Appl Appl Sequence 32, Appl Sequence 32, Appl Appl Sequence 32, Appl Appl Appl Sequence 32, Appl Appl Appl Appl Appl Appl Appl App		7 THE THERAPY	1; Length 448; 8; Indels 0; Gaps 0;	MSGSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60	DSDLSDPWWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120 	SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPP 180 	PQGAVIRAMPVYKRAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
US-09-277-196-20 US-09-081-975-3 US-09-027-580-2 US-08-047-0418-27 US-08-390-515A-8 US-08-390-515A-8 US-08-697-221-17 US-08-097-221-17 US-08-047-041A-25 US-08-347-792-2 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7 US-08-390-516C-7	ALIGNMENTS	IS/09643597 1. D. Naya S. 2. A.W. Cata D. Scila D. Sirul S	; Score 2383; DB 4, ; Pred. No. 3.6e-218 0; Mismatches 0	IMDFLEQPICSVQPIDLNF' 	NSMDQQIQNGSSSTSPYNTI 	DVSFQQSSTAKSATWTYSTI 	TEVVKRCPNHELSREFNEG(
54.4 54.4 30.3		ation [Jun Jun Jun Jun Jun Jun Jun Ju	th 100.08 Similarity 100.08 48; Conservative	MSQSTQTNEFLSPEVFQH 	DSDLSDPMWPQYTNLGLL 	SPSPAIPSNTDYPGPHSF 	PQGAVIRAMPVYKKAEHV
28 1297.5 29 1297.5 30 753.5 31 722.5 32 722.5 34 722.5 36 717.5 36 717.5 40 717.5 41 717.5 42 717.5 43 717.5 44 717.5		RESULT 1 US-09-643-597-340 Sequence 340, Applics Patent No. 6426072; GENERAL INFORMATION: APPLICANT: Wang, TC APPLICANT: Fan, Lif APPLICANT: HOSKEN, APPLICANT: Wang, TC APPLICANT: Wang, TC APPLICANT: Wang, TC APPLICANT: HOSKEN, APPLICANT: HOSKEN, APPLICANT: HOSKEN, APPLICANT: MANG, APPLICANT: TI, Sam, APPLICANT: MANG, APPLICANT: HOGERS, APPLICANT: MANGILL TITLE OF INVENTION: FILE REFERENCE: 21G CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION CURRENT FILING DATE NUMBER OF SEQ ID NOS SEQ ID NO 340 LENGTH: 448 TYPE: PRT T	Query Match Best Local S. Matches 448	Qy 1.1 Db 1.1	Qy 61 1 Db 61 1	Oy 121 9	Qy 181 DD 181 DD
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Mismatches
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CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0
 LVEPRRETPKQSDVFFRHSKPPNRSVYP
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                                                                                                                 APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaltanya
                                                                                                                                                                                Fanger, Gary R.
Li, Samuel X.
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Best Local Similarity 100.
Matches 448; Conservative
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APPLICANT: Wang, Aijun
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                                                             US-09-606-421B-340
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US-09-643-597-344
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APPLICANT:
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GENERAL INFOGRATION:
APPLICANT: Wang, Tongtong
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Banger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOI
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAI,
FILE REFERENCE: 210121.455C8
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 340
LENGTH: 448
                                                                                                                                         LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
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                                                                                                                                                                                                                             ; Sequence 340, Application US/09542615A; Patent No. 6518256; GENERAL INFORMATION:
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APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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                                                                                                                                                                                                                                                                                          Score 2383; DB 4;
Pred. No. 3.6e-218;
                                         AND DIAGNOSIS OF LUNG CANCER
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121 SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPP 180
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APPLICANT: Skeiky, Yasir A.W.
ATTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121 455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
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Pred. No. 3.1e-199;
3; Mismatches 7;
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C8
                                                                                   FastSEQ for Windows Version 3.0
                           CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: L. Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
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Best Local Similarity 94.1%;
Matches 416; Conservative
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SEQ ID NO 344
LENGTH: 516
TYPE: PRT
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LENGTH: 516
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                     APPLICANT: Raid, Argan,
APPLICANT: Raid, Argan,
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Mang, Aljun
APPLICANT: McMedill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455c11
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: LENCTH: 516
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APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                               Score 2185; DB 4;
Pred. No. 3.1e-199;
3; Mismatches 7;
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            Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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94.1%;
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Matches 416; Conservative
Wang, Tongtong
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US-09-643-597-344
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Pred. No. 4.3e-199;
3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Falo, Ligun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
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Best Local Similarity 94.1%;
Matches 416; Conservative
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US-09-542-615A-339
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US-09-542-615A-339
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SEQ ID NO 339
LENGTH: 641
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Rang, Wichael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Cary R.
APPLICANT: Applicant: Samuel X.
APPLICANT: Nang, Aljun
APPLICANT: Mang, Aljun
APPLICANT: Model X.
APPLICANT: 
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                                                                  Score 2185; DB 4;
Pred. No. 3.1e-199;
3; Mismatches 7;
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                                                                       91.7%;
94.1%;
                                                                     Query Match
Best Local Similarity 94.1
Matches 416; Conservative
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; ORGANISM: Homo sapiens
US-09-606-421B-344
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US-09-643-597-339
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Matches 416; Conserv
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosker, Nancy
APPLICANT: Hosker, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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Pred. No. 4.7e-199;
3; Mismatches 7;
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FastSEQ for Windows Version 3.0
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                                                                                                                                                                                      Sequence 342, Application US/09643597
Patent No. 6426072
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Best Local Similarity 94.1%;
Matches 416; Conservative
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Fan, Ligun
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US-09-643-597-342
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APPLICANT:
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Kanger, Aljun
APPLICANT: Washer, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/666,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
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94.1%; Pred. No. 4.3e-199;
iive 3; Mismatches 7;
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Matches 416; Conservative
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; ORGANISM: Homo sapiens
US-09-606-421B-339
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US-09-606-421B-339
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Michael D.
                                Hosken, Nancy
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APPLICANT: Fan, Liqun
APPLICANT: Alos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2185; DB 4;
Pred. No. 4.7e-199;
3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 3.0
                                                                                                        Sequence 342, Application US/09542615A Patent No. 6518256 GENERAL INFORMATION:
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421 LVEPRRETPKQSDVFFRHSKPP 442
                           --- OTSIQSPSSYGNSSPP 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 LVEPRRETPKQSDVFFRHSKPP 442
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Best Local Similarity 94.1%;
Matches 416; Conservative
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US-09-542-615A-342
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                                                                APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REPRENDE: 210121.455C9
CURRENT APPLICATION UNDER: US/09/606,421B
CURRENT APPLICATION UNDER: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6476206
GENERAL INFORMATION:
APPLICANT: Trink, Barry
APPLICANT: Trink, Barry
APPLICANT: Ratovitski, Edward
APPLICANT: Ratovitski, Edward
APPLICANT: Ratovitski, David
TITLE OF INVENTION: p40 Protein Acts as an Oncogene
FILE REFERENCE: 01107.79765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2185; DB 4;
Pred. No. 4.7e-199;
3; Mismatches 7;
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CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/079736
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 20
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94.18;
Bangur, Chaitanya
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Best Local Similarity 94.19
Matches 416; Conservative
                                                Fanger, Gary R.
Li, Samuel X.
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 Query Match
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APPLICANT: Wang, Tongtong
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Enger, Gary R.
APPLICANT: Li, Samuel J.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Meng, Aljun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Howenil, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210.21.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION NOMBER: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 426;
                                                                                              89.6%; Score 2136; DB 4;
.larity 93.1%; Pred. No. 1e-194;
Conservative 5; Mismatches 9;
SOFTWARE: FastSEQ for Windows Version 3.0
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                                      TYPE: PRT
CORGANISM: Homo sapiens
US-09-277-196-19
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US-09-643-597-343
                                                                                                           Best Local Similarity
Matches 405; Conserv
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           SEQ ID NO 19
LENGTH: 426
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                                                                                  70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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                                    16;
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 Length 461;
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Patent No. 6518256
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Narcy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAE;
TITLE OF INVENTION: COMPOUNDS.
FILE REFERENCE: 210121.455C8
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Pred. No. 6.2e-164;
3; Mismatches 7;
   ; DB 4;
6.2e-164;
Score 1813; DE
Pred. No. 6.2e-
3; Mismatches
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                                3;
76.1%;
93.0%;
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Best Local Similarity 93.0%;
Matches 347; Conservative
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                                Matches 347; Conservative
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                 Similarity
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US-09-542-615A-343
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Qy	250 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP 309
qa	195 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP 254
O _y	310 GRDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTHGIQMTSIKKRRSPDDELLYLPVRGR.369
QQ	255 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 314
Qy	370 ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP 429
qq	315 ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQQQHULLQKQTS 358
Qy	430 KOSDVFFRHSKPP 442
qa	359 IQSPSSYGNSSPP 371
Search Job tim	Search completed: August 7, 2003, 09:54:52 Job time : 13.3586 secs

OM protein - protein search, using sw model

August 7, 2003, 09:46:34; Search time 19.1264 Seconds Run on:

(without alignments)
2781.719 Million cell updates/sec

US-09-538-106-15

2383 1 MSQSTQTNEFLSPEVFQHIW.....PKQSDVFFRHSKPPNRSVYP 448 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 451899 seqs, 118759770 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published_Applications_AA:* Database :

/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:

ptodata/1/pubpaa/US09B_PUBCOMB.pep:* /ptodata/1/pubpaa/US09C_PUBCOMB.pep:* /ptodata/1/pubpaa/US09_NEW_PUB.pep:* /ptodata/1/pubpaa/US10A_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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/ptodata/1/pubpaa/US60_NEW_PUB.pep:* otodata/1/pubpaa/US10B_PUBCOMB.pep: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

/cqn2_6,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 340, App	Sequence 340, App	Sequence 340, App	Sequence 344, App	Sequence 344, App	Sequence 344, App	Sequence 339, App	Sequence 339, App	Sequence 339, App	Sequence 342, App	Sequence 342, App	Sequence 342, App	Sequence 19, Appl	Sequence 343, App	Sequence 343, App
	ID	US-09-735-705-340	0 US-09-850-716A-340	0 US-09-897-778-340	US-09-735-705-344	O US-09-850-716A-344				0 US-09-897-778-339	US-09-735-705-342	0 US-09-850-716A-342	0 US-09-897-778-342	5 US-10-274-874-19	US-09-735-705-343	J US-09-850-716A-343
	Query Match Length DB	448 9	448 10	448 10	516 9	516 10		٠.	641 10	_	6 089	680 10	680 10	426 15	461 9	461 10
ф	Query Match I	100.0	100.0	100.0	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	9.68	76.1	76.1
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Sequence 343, App	Sequence 341, App	Sequence 341, App	Sequence 2, Appli	Sequence 338, App	Sequence 338, App	Sequence 338, App	Sequence 152, App	6)	Sequence 152, App	Sequence 152, App	Sequence 20, Appl	Sequence 3, Appli		Sequence 32, Appl	Sequence 3, Appli			Seguence 9, Appli								4	ñ	Sequence 28, Appl
US-09-897-778-343 US-09-735-705-341		US-09-897-778-341	US-10-274-874-2	US-09-735-705-338	US-09-850-716A-338	US-09-897-778-338	US-09-735-705-152	US-09-850-716A-152	US-09-897-778-152	US-09-466-396A-152	US-10-274-874-20	US-10-155-059-3	US-09-732-384-10	US-09-776-695-32	US-09-732-384-3	US-09-860-211-9		US-09-860-286-9										US-09-968-851-28
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76.1	75.4	75.4	75.4	75.4	75.4	75.4	75.1	75.1	75.1	75.1	54.4	54.4	54.4	30.1	30.1	30.1	30.1	30.1	30.1	30.1	30.1	30.1	30.0	30.0	29.8	29.6	29.5	29.0
1813 1796	1796	1796	1796	1796	.1796	1796	1789	1789	1789	1789	1297.5	1297.5	1297.5	717.5	717.5	717.5	717.5	717.5	717.5	717.5	717.5	716.5	714	714	711	704.5	704	690.5
16	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

THE THERAPY APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Banger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419 FastSEQ for Windows Version 3.0 Sequence 340, Application US/09735705 Patent No. US20020052329A1 ŝ Kalos, Michael D. Bangur, Chaitanya Hosken, Nancy Skeiky, Yasir A.W Fanger, Gary R. Li, Samuel X. Wang, Tongtong Fan, Liqun Wang, Aijun ORGANISM: Homo sapiens GENERAL INFORMATION: US-09-735-705-340 US-09-735-705-340 SEQ ID NO 340 LENGIH: 448 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT

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Query Match 100.0%; Score 2383; DB 9; Length 448; Best Local Similarity 100.0%; Pred. No. 1e-208; Matches 448; Conservative 0; Mismatches 0; Indels 0;

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	301	361	SULT 3	8-3 40, US	; APPLICANT: Wang, Tongtong ; APPLICANT: Marnerakis, Margarita ; APPLICANT: Fanger, Gary R. ; APPLICANT: Vedvick, Thomas S.	; APPLICANT: Carter, Darrick ; APPLICANT: Watanabe, Yoshihiro ; APPLICANT: Henderson, Robert A. ; APPLICANT: Peckham, David W. ; APPLICANT: Fanger. Neil	INV INV REN PPL	: 467 r Windows	; LENGTH: 448 ; TYE: PRT ; ORGANISM: Homo sapiens US-09-897-778-340	Query Match 100.0%; Score 2383; DB 10; Length Best Local Similarity 100.0%; Pred. No. 1e-208; Matches 448; Conservative 0; Mismatches 0; Indels	QY 1 MSOSTQTNEFLSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSEDGATNK	Qy 61 DSDLSDPWMPQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSP	121	Qy 181 PQGAVIRAMPVIKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVE	241	Qy 301 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMT	Qy 361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQHQHLLQ
QY 61 DSDLSDPMWPQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120 	QY 121 SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180	QY . 181 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240	OY 241 ITGROSVLUPYEPPQVGTEFTTVLXNEWCNSSCVGGMNRRPILLIIVTLETRDGQVLGRRC 300	QY 301 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360 	QY 361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQQQQQQQQCQQQQQQQQQQQQQQQQQQQQQ	OY 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448 	RESULT 2 US-09-850-716A-340 ; Sequence 340, Application US/09850716A ; Patent No. US20020115139A1	GENERAL INFOR APPLICANT: R APPLICANT:	AFFICANT: RELUEL: MATC WITHOUS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSIS OF LUNG CANCER FILE REPRENEUE: 210121.45515 CIRDDAW ADDITION: MATCHER, 1670,060 7158	U.	; TIVE: PRT ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-850-716A-340	Query Match 100.0%; Score 2383; DB 10; Length 448; Best Local Similarity 100.0%; Pred. No. 1e-208; Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	EPSEDGATNKIEISMD 	Qy 61 DSDLSDPMWPQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120	Qy 121 SPSPAIPSNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPP 180	OY 181 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240	Qy 241 ITGRQSVLVPYEPPQVGTEFTTVLXNFWCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC 300

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RESPYAQPSSTEDAL 120
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WITSIKKRRSPDDE 360
                 LLOKHLLSACFRNE 420
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LETRDGQVLGRRC 300
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%; Score 2185; DB 9; Length 516;
larity 94.1%; Pred. No. 1.4e-190;
Conservative 3; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                         THE THERAPY
                                                                                                                             APPLICANT: Rauls, Augus APPLICANT: Ralos, Michael D. APPLICANT: Ralos, Michael D. APPLICANT: Bangur, Chaltanya S. APPLICANT: Bangur, Chaltanya S. APPLICANT: Bosken, Nancy APPLICANT: Fanger, Gary R. APPLICANT: Fanger, Gary R. APPLICANT: Wang, Aijun APPLICANT: Weng, Aijun APPLICANT: Henderson, Robert A. APPLICANT: Moneill, Particia D. APPLICANT: Moneill, Particia D. APPLICANT: Panger, Neil TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C14 CURRENT APPLICATION NUMBER: US/09/735,705 CURRENT FILING DATE: 2000-12-12 NUMBER OF SEQ ID NOS: 419 SOFTWARE: EastsED for Windows Version 3.0 SEQ ID NO 344 LENGTH: 516
              LVEPRRETPROSDVFFRHSKPPNRSVYP
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Patent No. US20020052329A1
GENERAL INFORMATION:
                                                                                                                    Wang, Tongtong
Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-09-735-705-344
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Matches 416; Conserv
                                                           RESULT 4
US-09-735-705-344
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Sequence 344, Application US/09850716A

Patent No. US20020115139A1

SEGNERAL INRORMATION:
APPLICAWE: Kalos, Michael D.
APPLICANT: Relos, Michael D.
APPLICANT: Releter, Marc W.
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REPERENCE: 210121.455C15
CURRENT RAPLICATION NUMBER: US/09/850,716A

CURRENT PILLICATION NUMBER: 2001-05-07

NUMBER OF SEQ ID NOS: 440
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APPLICANT: Peckham, David W.
APPLICANT: Fanger, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 1.4e-190;
3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
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94.1%;
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Best Local Similarity 94.1;
Matches 416; Conservative
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                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 344
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TYPE: PRT
ORGANISM: HOMO
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                                                                         US-09-735-705-339
           LENGIH: 641
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APPLICANT: Fail, Light
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Weakly, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Morbill, Patricia D.
APPLICANT: Composition of the composit
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Pred. No. 1.4e-190;
3; Mismatches 7;
FILE REFERENCE: 210121.455C16
CURRENT PPLICATION NUMBER: U5/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTHARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 344
LENGTH: 516
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Patent No. US20020052329A1
GENERAL INFORMATION:
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Best Local Similarity 94.1%;
Matches 416; Conservative
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Fan, Ligun
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US-09-897-778-344
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                                                     Score 2185; DB 9;
Pred. No. 2e-190;
3; Mismatches 7;
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APPLICANT: MoMeill, Patricia D.
APPLICANT: MCHELEL, MATC W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT APPLICATION NUMBER: US/09/850,716A
SOFTWARMER FESTERED FOR WINDOWS VERSION 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
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                                                   Query Match
Best Local Similarity 94.1
Matches 416; Conservative
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; ORGANISM: Homo sapiens
US-09-735-705-342
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US-09-735-705-342
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TYPE: PRT
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                    DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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APPLICANT: Warnerakis, Margarita
APPLICANT: Marnerakis, Margarita
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Toninick
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: OMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 2e-190;
3; Mismatches 7;
                                                                                                                                                                                                                                                                      421 LVEPRRETPKQSDVFFRHSKPP 442
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Best Local Similarity 94.1%;
Matches 416; Conservative
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US-09-897-778-339
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LENGTH: 641
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                                                                                                                                                                             APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Moneill, Particia D.
APPLICANT: Moneill, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
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Pred. No. 2.1e-190;
3; Mismatches 7;
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Patent No. US20020052329A1
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Best Local Similarity 94.1%;
Matches 416; Conservative
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Bangur, Chaitanya
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Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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US20020147143A1
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Patent No. US2020115139A1

GENERAL INFORMATION:

APPLICANT: Ralos, Michael D.

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER

FILE REFERENCE: 210121.455C15

CURRENT APPLICATION NUMBER: US/09/850,716A

NUMBER OF SEQ 1D NOS: 440

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                          421 LVEPRRETPKQSDVFFRHSKPP 442
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                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-850-716A-342
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US-09-897-778-342
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                                                               APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wedvande, Yoshihiro
APPLICANT: Wedvande, Yoshihiro
APPLICANT: Wenderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Penger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
TITLE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SEQ ID NO 342
LENGTH: 680
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Pred. No. 2.1e-190;
3; Mismatches 7;
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Publication No. US20030113774A1
GENERAL INFORMATION:
APPLICANT: Trink, Barry
APPLICANT: Tarink, Barry
APPLICANT: Ratovitski, Edward
APPLICANT: Sidransky, David
ITILE OF INVENTION: P40 Protein Acts as an C
FILE REPERENCE: 01107.79765
CURRENT APPLICATION NUMBER: US/10/274,874
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APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
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Best Local Similarity 94.1%;
Matches 416; Conservative 3
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US-09-897-778-342
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FastSEQ for Windows Version 3.0
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Best Local Similarity 93.0%;
Matches 347; Conservative
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359 IQSPSSYGNSSPP 371
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Matches 347; Conservative
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US-09-850-716A-343
                                                             Homo sapiens
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US-09-850-716A-343
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LENGTH: 461
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APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bongur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Edsen, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mang, Aljun
APPLICANT: Panger, Nebert A.
APPLICANT: Panger, Nell
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF STORY APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                    Length 426;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                   Score 2136; DB 15;
Pred. No. 3.1e-186;
5; Mismatches 9;
         PRIOR APPLICATION NUMBER: U$/09/277,196
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079736
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 3.0
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 2002-10-22
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Best Local Similarity 93.1%;
Matches 405; Conservative
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Fan, Liqun
                                                                                                                                                   ORGANISM: Homo sapiens
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-09-735-705-343
                                                                                                                                                                       US-10-274-874-19
                                                                                                                         LENGTH: 426
                                                                                                         SEQ ID NO 19
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                                                                                 70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
                                                                                                                                                                                                                                                                         135 PVYKKABHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
                                                                                                                                                                                                                                                                                                                                                                        254
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                                                                                                                                                                                                                                                   PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                   250 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                      310 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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Length 461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: MCHEILL, PATTICIA D.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FITLE FREPERCE: 210121.455015
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-5-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASISEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1813; DB 10;
Pred. No. 9.8e-157;
3; Mismatches 7;
76.1%; Score 1813; DB 9; 93.0%; Pred. No. 9.8e-157; iive 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 343, Application US/09850716A; Patent No. US20020115139A1
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Qy	190	190 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
qa	135	PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
Qγ	250	14 -
qa	195	PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP 254
Οy	310	310 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 369
qq	255	GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 314
Οy	370	370 ETYEMLLKIKESLELMOYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP 429
qq	315	ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTS 358
ΟΥ .	430	430 KOSDVFFRHSKPP 442
Db	359	359 IQSPSSYGNSSPP 371
Search Job tim	comple:	Search completed: August 7, 2003, 09:57:08 Job time : 20.1264 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 7, 2003, 09:42:03; Search time 14.1241 Seconds Run on:

(without alignments)
3050.350 Million cell updates/sec

2383 1 MSQSTQTNEFLSPEVFQHIW......PKQSDVFFRHSKPPNRSVYP 448 US-09-538-106-15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: piri: * 2: pir2: * 3: pir3: * 4: pir4: * PIR_76:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Descrip	cellular tumor ant	tumor	tumor	cellular tumor ant	tumor suppressor p	cellular tumor ant	tumor suppressor p	=	Bassoon protein -	hypothetical prote	transcription fact	proline-rich pepti	polyketide synthas	DHR39-short protei	nuclear steroid/th	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	hypothetical prote	₽	syndecan precursor		flocculation suppr	hypothetical prote					
. 0	JH0631	A29376	S02193	S51648	S02192	JH0633	DNHU53	DNMS53	806594	JC6176	S38824	JC6193	146226	T42730	T32008	A56923	A41819	C69679	833709	S33708	D54689	C54689	A56178	T31782	A56922	A54949	149528	S61694	T06635
DB	-	Н	Н	-	Н	Н	-	-	-	N	~	~	7	7	7	7	~	~	-		-	7	~	7	7	7	~	Н	7
Length	396	363	367	386	391	396	393	390	393	393	381	391	77	3942	1819	2529	5762	4273	701	808	1691	1894	1912	631	2578	395	384	166	606
% Query Match	35.6	32.6		31.1	٠.	30.2		30.0				•		4.8	4.7	4.6	4.6	4.6	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4
ŭ	847.5	777.5	764.5	741.5	732	719.5	717.5	715	714.5	704	702	699.5	259.5	114.5	111.5	110.5	110	109	108.5	108.5	107	107	107	106.5	106.5	105.5	105	105	105
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PGRDRKADEDSIRKQQ----VSDSTKNGDGTKRPFRQ-NTHGIQMTSIKKRRS----PDDE 360

309

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LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 399 : | :||:| |||| | :|||| : :| : ||||: 327 IYTLQIRGKEKYEMLKKFNDSLELSELVPVADADKYRQK 365

361

SNF2 protein · yea LTR gag/pol polypr	protein C43Ell.3 hypothetical prote HF-l regulatory el	mycelial surface a hypothetical prote	hypoxia-inducible hypothetical prote	nypocnecical prote GTPase-activating A-kinase anchor pr	Bassoon protein - hypoxia-inducible	hypothetical prote zinc finger protei
S15047 T01397	B87754 T00344 A48143	T17415 S19150	JC4851 T24447	T513/2 S27809 T03094	T42761 JC7619	T15264 T14273
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1703	1590 1533 780	1203 628	1505	1165 2359	3938 811	1621 1888
4.4	4 4 4 4	4.4	44.	444	4.2	4.2
104.5	104 103 102.5	102.5	100.5	9 9 9 9 9 9 9 9	99.5 99	6 6 6
30	3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	35 36	38	4 4 4 4 1	43 43	44 45

ALIGNMENTS

	RESULT 1 JH631 cellular tumor antigen p53 - rainbow trout C.Species: Oncorhynchus mykiss (rainbow trout) C.Species: Oncorhynchus mykiss (rainbow trout) C.Species: Oncorhynchus mykiss (rainbow trout) C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C.Accession: JH631 R.de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T. Gene 112, 241-245, 1992 A.Title: Rainbow trout p53: cDNA cloning and biochemical characterization. A.Title: Rainbow trout p53: cDNA cloning and biochemical characterization. A.Reference number: JH0631 A.Molecule type: mRNA A.Residues: 1-396 < CDEF> A.Cross-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829 A.Cross-references: GB:M75145; NID:g213828 A.Cross-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829 A.Cross-references: GB:M75145; NID:g213829 A.Cross-references: GB:M75145; NID:g213829 A.Cross-references: GB:M75145; NID:g213829 A.Cross-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829 A.Cross-references: GB:M75145; NID:g213829 A.Cross-references: GB:M75145; NID:g21
	Query MatCn Best Local Similarity 45.4%; Pred. No. 7.5e-58; Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;
<u> </u>	QY 11 LSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDEMWP 70
	QY 71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDALS-PSPAIPS 128
<u> </u>	QY 129 NIDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRA 188 :
<u> </u>	QY 189 MPVYKKAEHVTEVVKRCPNHELSREFNEGGIAPPSHLIRVEGNSHAQYVEDPITGRQSVL 248 :: : :

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C;Accession: S51648
R;Pequiedt, F.; Willems, L.; Burny, A.; Kettmann, R.
submitted to the EMBL Data Library, September 1994
A;Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and it A;Reference number: S51648
A;Accession: S51648
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-386 <DEO>
                                                Cypecies: Gallus gallus (chicken)
Cypecies: Gallus gallus (chicken)
Cypecies: Gallus gallus (chicken)
Cypecies: 302193
Cypecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CyAccession: 302193
CyCoussi, T.; Beque, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
A.Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
A.Feference number: 302193
A.Feference number: 302193
A.Molecule type: MRNA
A.Ccession: 302193
A.Ccession: 502193
A.Ccoss references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741
C;Superfamily: cellular tumor antigen p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho F;161,164,224,228/Bahding site: zinc (Cys, His, Cys, Cys) #status predicted
F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
A;Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
C;Superfamily: cellular tumor antigen p53
C;Superfamily: cellular tumor antigen p53
C;Seywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote F;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) **status predicted F;385/Binding site: phosphoryl-RNA (Ser) (covalent) **status predicted
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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 AVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 PYEPPEVGSDCTTVLYNPMCNSSCMGGMNRRPILITILTLEGPGGQLLGRRCFEVRVCACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LSP-EVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 LEPTEVFMDLWSMLPY---SMOOL-----PLPEDHSNWQELS----PLEPSDPPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.1%; Score 764.5; DB 1; Best Local Similarity 44.6%; Pred. No. 1.8e-51; Matches 169; Conservative 50; Mismatches 105;
                                N; Alternate names: nuclear oncoprotein p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || ||||| :| |:|:| :
GRRRYEMLKEINEALQLAE 335
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cellular tumor antigen p53 - chicken
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C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph
F;150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                             proteir
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R;Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.
Oncogene 9, 109-120, 1994
A;Title: Overaxpression of Wild-type p53 interferes with normal development in Xenopus A;Reference number: 151639; MUID:94134403; PMID:8302570
                                                                                                                                                                                                                                                                                                A;Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a A;Reference number: A29376; MUID:88143684; PMID:2830576
A;Accession: A29376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTF 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRCFEARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKR 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                    cellular tumor antigen p53 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Secession: A29376; S61531; S72313; I51639
C;Accession: A29376; S61531; C.C.; Mechali, M.; May, P.; Kress, M.
Oncogene 1, 71-78, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-293,295-363 <HOE>
A;Cross-réferences: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
A;Cross-réferences: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
R;Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, W.
submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQSTQTNEFLSPEVFQHIWDFLEQPI ----CSVQPIDLNFVDEPSEDGATNKIEISMDCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSETGMDPPLSQETFEDLWSLLPDPLQTVTCRLDNLS-EFPDYP-----LAADMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AVPTVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-51,'S',53-70,72-293,295-363 <HOW>
A;Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 32.6%; Score 777.5; DB 1; Length 3 Best Local Similarity 42.5%; Pred. No. 1.7e-52; Matches 171; Conservative 55; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R---SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 VLQE-----GLMGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S72313
A; Accession: S72313
                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-363 <SOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S61531
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Length 386;

DB 1;

Score 741.5;

31.1%;

Query Match

RESULT S02193

Best Local Similarity 38.4%; Pred. No. 1.1e-49; Matches 165; Conservative 68; Mismatches 126; Indels 71; Gaps 11;	qq	: : : 3
QY 11 LSPEVPOHIMDFLEQPICSVQPIDLANFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMMP 70	Qy	61 DSDLSDPMMPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120 1
OY 71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA 125. Db 43 LLPYTDVATWLDECPNEAPQMPEPSAPAAPPPATPAPATSWPL 85	Qy Dp	121 SPSPAIPSNIDYPGPHSFDVSFQOSSTAKSATWIYSTELKKLYCQIAKICPIQIKVMTPP 180
QY 126IPSNIDYPGPHSFDVSFQSSTAKSAIWTYSTELKKLYCOIAKTCPIQIKVWIPPPQ 182	Qy	181 PQGAVIRAMPVYKRAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEGNSHAQYVED 239
QY 183 GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGGIAPPSHLIRVEGNSHAQYVEDPIT 242 : : : : : :	Qy	240 PITGRQSVLVPEPPQVGTEFTTVLXNEMCNSSCVGGMNRRPILLIVTLETRDGQVLGRR 299 1
QY 243 GRQSVLVPYEPPQVGTEFTTVLXNEMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFE 302	Qy	300 CFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-D 358
QY 303 ARICACPGRDARADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDEL 361	oy Bb	359 DELLYLPVRGRETYEMLLKIKESLEL 384
Qy 362 LYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQH-OHLLQKHLLS-ACFRN 419	RESULT 6 JH0633	
Qy 420 ELVEPRRETP 429 bb 376 PMLKREGP 383	cellular to N; Alternato C; Species: C; Date: 10	cellular tumor antigen p53 - golden hamster NAthternate names: tumor-suppressor protein p53 C.Species: Mesocricetus auratus (golden hamster) C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
RESULT 5 S02192 cellular tumor antigen p53 - rat	C; Access R; Legros Gene 112 A; Title: A; Referen	C;Accession: JH0b33 R;Legros, Y.; McIntyre, P.; Soussi, T. Gene 112, 247-250, 1992 A;Title: The cDNA cloning and immunological characterization of hamster p53.
C.Species: Rattus norvegicus (Norway rat) C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C.Accession: S02192; S41149	A; Molecu A; Residue A; Cross	M75144;
Nucleic Acids Res. 16, 11384, 1988 A;Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein. A;Reference number: S02192; MUID:89083585; PMID:3060862 A;Accession: S02192.	A) Experi C; Genetic A) Gene: [C; Superf C; Keyword	Experimental Source: Kloney, Strain Mri Genetics: Gene: p53 Superfamily: cellular tumor antigen p53 Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
A;Molecule type: mRNA A;Residues: 1-391 <sou> A;Cross-references: EMBL:X13058; NID:q56828; PIDN:CAA31457.1; PID:q56829</sou>	F; 179, 18; F; 395/Bir	ng site: zinc (Cys, His, Cys, Cys) #status predicted sphoryl-RNA (Ser) (covalent) #status predicted
R;Hulla, J.E.; Schneider, R.P. Nucleic Acids Res. 21, 713-717, 1993 A;Title: Structure of the rat p53 tumor suppressor gene. A:Ritcher Structure of the Armon Suppressor gene.	Query Match Best Local Matches 16	Match 30.2%; Score 719.5; DB 1; Length 396; Local Similarity 38.1%; Pred. No. 6e-48; Local Similarity 67; Mismatches 145; Indels 51; Gaps 8;
A; Accession: S41149 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA	Qy Dp	11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPWWP 70
A; Residues: 1-173, W/, 175-391 < HUL> A; Cross-references: EMBL:L07909 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992 C; Genetics:	Qy	71 QYTNLGLLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNT 130 1
A;Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph F;174,177,286,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;39(/Rinding site: phosphoryl-RNA (Sar) (Consent) #eratus predicted	QY	131 DYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAMP 190 : :
Query Match 30.7%; Score 732; DB 1; Length 391; Best Local Similarity 42.0%; Pred. No. 6.3e-49. Matches 162; Conservative 64; Mismatches 116; Indels 44; Gaps 11;	Q _Y	191 VYKKAEHVTEVVKRCPNHELSREFNEGGIAPPSHLIRVEGNSHAQYVEDPITGROSVLVP 250 :{ : :: : :
LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 6	oy yo	251 YEPPQYGTEFTTVL/NEWCNSSCVGGMNRRPILLITYLETRDGQVLGRRCFEARICACPG 310

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A; Rosiduces: 1-71, 'P', 73-272, 'H', 274-393 (HAR>
A; Rosiduces: 1-71, 'P', 73-272, 'H', 274-393 (HAR>
A; Cross-references: GB:K03199; NID:g189478; PIDN:AAA59989.1; PID:g189479
A; Cross-references: GB:K03199; NID:g189478; PIDN:AA531
R; Harris, N.; Brill, E; Shohat, O; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, V. Mol. Cell. Biol. 6, 4650-4656, 1986
A; Title: Molecular basis for heterogeneity of the human p53 protein.
A; Reference number: A93086; MUID:87089826; PMID:3025664
A; Accession: A25397
A; Molecule type: mRNA
A; Residuces: 1-76, TT, 80-393 <HAR1>
A; Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A; Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
A; Molecule type: mRNA
A; Residuces: 1-71, Pr, 73-78, TT, 80-393 <HAR2>
A; Molecule type: mRNA
A; Residuces: 1-71, Pr, 73-78, TT, 80-393 <HAR2>
A; Molecule type: mRNA
A; Residuces: 1-71, Pr, 73-78, TT, 80-393 <HAR2>
A; Molecule type: mRNA
A; Residuces: 1-71, Pr, 73-78, TT, 80-393 <HAR2>
A; Molecule type: mRNA
A; Residuces: 1-71, Pr, 73-78, TT, 80-393 <HAR2>
A; Molecule type: mRNA
A; Residuces: 1-71, Pr, 73-78, TT, 80-393 <HAR2>
A; Molecule type: mRNA
A; Residuces: 1-71, Pr, 73-78, TT, 80-393 <HAR2>
A; Molecule type: mRNA
A; Residuces: 1-71, Pr, 73-78, TT, 80-393 <HAR2>
A; Molecule type: mRNA
A; Residuces: 1-71, Pr, 73-78, TT, 80-393 <HAR2>
A; Molecule type: mRNA
A; Residuces: 1-71, Pr, 73-78, TT, 80-393 <HAR2>
A; Molecule type: mRNA
A; Residuces: Clone p53-H-19, transformed hybridoma SV-80 cell line
B; Matlashewski, G.J.; Tuck, S.; Pilm, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
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A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189, 'LESILSEWKEICVWSIWMTETLEDIVWWCPMSRLRIALT', 'VPPSTTTCVTVPAWAA'
A;Cross-references: EMBL;X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
A;Note: deletion of a C nucleotide causes a frameshift at position 566
A;Accession: 138083
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A;Molecule type: mRNA
A;Residues: 1-247,'Q',249-393 <F06>
A;Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PID:g506443
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A;Residues: 1-71,'P',73-237,'Y',239-393 <F07>
A;Cross-references: EMBL:X60016; NID:9506444; PIDN:CAA42631.1; PID:9506445
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A;Molecule type: mRNA
A;Residues: 1-192,'R',194-393 <F02>
A;Cross-references: EMBL:X60011; NID:9506434; PIDN:CAA42626.1; PID:9506435
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A;Accession: 138085
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A;Molecule type: mRNA
A;Realdues: 1-245, TT', 247-393 <F04>
A;Coss.references: EMBL:X60013; NID:9506438; PIDN:CAA42628.1;
A;Accession: I38086
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A;Molecule type: mRNA
A;Residues: 1-236, 1'. 238-393 <F05>
A;Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1;
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A;Molecule type: mRNA
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A;Status: translated from GB/EMBL/DDBJ
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A;Accession: $42669
A;Accession: $4261
A;Accession: $42837
A;
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N'Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Homo saplens (man)

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A;Residues: 1-393 <LAM>
A;Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1; PID
R;Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
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A:Title: A variation in the structure of the protein-coding region of the human p53 gene
A:Reference number: JT0436; MUID:89108008; PMID:2905688
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A; Residues: 1-71, Pv' 73-393 <2AK>
A; Residues: 1-71, Pv' 73-393 <2AK>
A; Cross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210
B; Harlow, E.; Williamson, N.W.; Ralaton, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
A; Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular in A; Reference number: A55060; MUID:85267676; PMID:3894933
                                                                                                                                                                                                                                                               RDRRTEEKNFQKKGEPCPELPPKSAKRALPINT---SSSPOPKRKTLDGEYFTLKIRGOE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::| :: |:|| :: |:|| 340 RFKMFQELNEALELKDAQALKASEDSGAHSSYLKSKKGQSASRLKKLMI------388
223 YEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTITLEDPSGNLLGRNSFEVRICACPG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                     371 TYEMLLKIKESLELMQYLPQHTIE-----TYRQQQQQQHQHLLQKHLLSACFRNELVEP 424
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A; Residues: 1-71, '7-73-393 <BUC2>
A; Cross-references: EMBL: M22898; MID: 9189474; PIDN: AAA59988.1; PID: 9189476
A; Note: this 72-Pro allele was found in both normal and malignant cell lines
R; Chumakov, P. M.; Almazov, V. P.; Jenkins, J. R.
submitted to the EMBL Data Library, August 1990
A; Reference number: $40773
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A;Residues: 1:393 <CHU>
A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
B;Matlashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol,
EMBO J. 3, 3257-3262, 1984
                                                                                                                                              RDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRE
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KREGP 393
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A;Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237; R;Chumakov, P.M.
Bioorg. Khim. 13, 1691-1694, 1987
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A; Moseidues: 1.159,7H'.161-167,7G',169-233,7T',235-390 <2AK>
A; Residues: 1.159,7H'.161-167,7GB:K01700; NID:953875
A; Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
Abl. Cell. Blol. 6, 3232-3239, 1986
A; Title: Immunologically distinct p53 molecules generated by alternative splicing.
A; Reference number: S38822; MUID:87064640; PMID:3023970
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28 Aug-1985 #sequence_revision 04-0ct-1996 #text_change 11-May-2000
C;Accession: A22739; S06336; A02684; S38823; S40014; I48703
R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
EMBO J. 3, 2179-2183, 1984
A;Title: Analysis of the gene coding for the murine cellular tumour antigen p53.
A;Reference number: A22739; MUID:85027173; PMID:6092064
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A;Reference number: S06336; MUID:88221682; PMID:3329909
A;Accession: S06336
                                                                                                                                                                                                                                                                                                                                                                                                                                            71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSP----SPAI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 PSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRV 157
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A;Title: A single gene and a pseudogene for the cellular tumour antigen p53. A;Reference number: A02684; MUID:84068204; PMID:6646235
A;Accession: A02684
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                                                                                                                                                                                                                                                                                                          14 LSQETFSDLWKLLPB-----NNVLSPLPSQAMDDLMLSPDDLEQWFTE--DP---
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                      Length 393;
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                Score 717.5; DB 1;
Pred. No. 8.4e-48;
); Mismatches 116;
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30.1%; Scor
41.2%; Pre-
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332 IRGRERFEMFRELNEALEL 350
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A; Residues: 1-134, 'V', 136-390 <CHU>
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                                                                                                                           Conservative
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A; Residues: 1-390 <ARA1>
                                                                              Similarity
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                      Query Match
Best Local Simi
Matches 156;
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A; Robecule type: mRNA
A; Realdues: 1-253, 0', 255-393 < F11.
A; Realdues: EMBL: 860020; NID: 9506452; PIDN: CAA42635.1; PID: 9506453
A; Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 1991
R; Futreal, P.A.; Barrett, J.C.; Waseman, R.W.
Nucleic Acids Res. 19, 6977, 1991
A; Title: An Alu polymorphism intragenic to the TP53 gene.
A; Recession: 138093; MUID: 92107726; PMID: 1762941
A; Accession: 138093; MUID: 92107726; PMID: 1762941
A; Accession: 138093
A; Status: translated from GB/EMBL/DDBJ
A; Residues: 1-393 < FUT>
A; Residues: 1-393 < FUT>
A; Residues: 1-393 < FUT>
A; Cross-references: EMBL: X54156; NID: 935213; PIDN: CAA38095.1; PID: 935214
A; Residues: 1-393 < FUT>
A; Tross-references: EMBL: X54156; NID: 935213; PIDN: CAA38095.1; PID: 935214
A; Title: D53 gene mutations in gastric cancer metastases and in gastric cancer cell line
A; Reference number: A44905; MUID: 92034678; PMID: 1933850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; CTOSS-references: GB:841977; NID:91679932; PIDN:AAB19325.1; PID:9232816
B; CTOSS-references: GB:841977; NID:94679932; PIDN:AAB19325.1; PID:9232816
A; CTOSS-references: GB:841977; NID:94036762; PMID:8221626
A; Reference number: 152681; MUID:94036762; PMID:8221626
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: 327-331, 'DGTSPQKENC' CHO>
A; Molecule type: 327-331, 'DGTSPQKENC' CHO>
A; Molecule type: 327-331, 'DGTSPQKENC' CHO>
A; Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymp
A; Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymp
Mol. Gen. Genet. 249, 425-431, 1995
A; Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragme
A; Reference number: S60151; MUID:96133682; PMID:8552047
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A) Residues: 246-247, W, 249-250 < YAM>
A) Rossidues: 246-247, W, 249-250 < YAM>
A) Rossidues: 246-247, W, 249-250 < YAM>
A) Rossidues: 246-247, W, 249-252 < YAM>
A) Rossidue extracted from NCB1 backbone (NCBIN:63157, NCBIP:63158)
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation NCB 1919
A) Note: mutation from a liver metastasis of a gastric cancer
A) Note: mutation NCB 1919

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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
B;Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
A;Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myb, N-myc, p53, HSP70,
                                                                                                                                                                   A.Accession: 138090
A.Status: translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A.Cross-references: EMBL:X60018; NID:9506448; PIDN:CAA42633.1; PID:950644§
A.Accession: 138091
A.Status: translated from GB/EMBL/DDBJ
A.Rolecule type: mRNA
A.Residues: 1-212, 'Q', 214-393 <F10>
A.Residues: 1-212, 'Q', 214-393 <F10>
A.Residues: 1-212, 'Q', 214-393 <F10>
A.Residues: L-212, 'Q', 214
                                                                   Residues: 1-247,'Q',249-393 <F08>
Cross-references: EMBL:X60017; NID:9506446; PIDN:CAA42632.1; PID:9506447
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us-09-538-106-15.rpr

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Cellular tumor antigen p53 - green monkey
C; Species: Cercopithecus aethiops (green monkey, grivet)
C; Species: Cercopithecus aethiops (green monkey, grivet)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: S06594
R; Rigaudy, P.; Eckhart, W.
Nucleic Acids Res, 17, 8375, 1989
A; Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p5
A; Reference number: S06594; MUID:90045967; PMID:2530498
A; Residues: 1-393 ~RIG>
A; Residues: 1-393 ~RIG>
A; Residues: 1-393 ~RIG>
A; Coss-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796
C; Superfamily: cellular tumor antigen p53
C; Superfamily: cellular tumor antigen p53
C; Reywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F; 176,179,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F; 392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
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A, Residues: 1-393 <LEE>
A, Cross-references: GB: U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230
C, Comment: This protein is a multimer, it plays the central role in a complex DNA iption, and recombination by protein/protein interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 PSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVI 186
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C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
C;Accession: JC6176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 ------LTEDPGPDEAPRMSEAAPH--MAPTP-AAPTPAAPAPAPSWPLSSSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSP----SPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 VLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 LSQETFSDLWKLLPE-----DLA--QW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
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Gene 184, 177-183, 1997
A;Title: Cloning and characterization of Chinese hamster
A;Reference number: JC6176; MUID:97183659; PMID:9031625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.0%; Score 714.5; DB 1; 41.2%; Pred. No. 1.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Mismatches 113;
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332 IRGRERFEMFRELNEALEL 350
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| :|: :|
371 GQSTSRHKKTMVK 383
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Best Local Si
Matches 156
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                                                                                                                                                                                                                                                                                                                                      A;Title: Cloning and expression analysis of full length mouse cDNA sequences encoding the A;Title: Cloning and expression analysis of full length mouse cDNA sequences encoding the A;Reference number: 148703; MUID:84272240; PMID:6379601
A;Accession: 148703
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residuae: 1-77, RY, 49-78, QW, 82-390 CRES>
A;Residuae: 1-77, RY, 49-78, QW, 82-390 CRES>
A;Cross-references: EMBL:X00741; NID:953570; PIDN:CAA25323.1; PID:953571
C;Comment: This DNA-binding protein plays an essential role in the regulation of cell dicycomment: The tetramer association region may exhibit a beta-turn, beta-sheet, beta-turn C;Superfamily: cellular tumor antigen psi C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein; F:1-44/Domain: transcription activation #status predicted cTRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted 173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted 1312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted 1389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 NSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLET 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEG 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---AHATEESGDSRAHSSYLKTKK 370
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                                             A; Cross-references: EMBL.M13873
R; Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter,
submitted to the EMBL Data Library, July 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SQSTQTNEF-LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMO
                                                                                                                                                              A; Accession: S40014
A; Molecule type: mRNA
A; Cross-references: EMBL: H13873; NID: 9200200; PIDN: AAA39882.1; PID: 9200201
R; Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
Nucleic Acids Res. 12, 5609-5626, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOSDISLELPLSQETFSGLWKLL------PPED-----ILPSPHC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.3%; Pred. No. 1.3e-47; ive 62; Mismatches 125; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;16-26/Region: conserved region I
F;99-289/Domain: DNA-binding core #status predicted <DBC>
                     A;Residues: 1-167,'G',169-233,'I',235-390 <ARA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.0%; Score 715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;233-248/Region: L3 loop
F;267-283/Region: conserved region V
F;313-319/Region: nuclear location signal
F;319-357/Region: tetramer association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;168-178/Region: conserved region III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;108-121/Region: L1 loop
F;114-139/Region: conserved region II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 QQQQQQHQHLLQK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 166; Conservative
                                                                                                                                            A; Reference number: S40014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;160-192/Region: L2 loop
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Best Local Similarity
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F;108-121/Region: L1 loop
F;114-139/Region: conserved region II
F;160-192/Region: conserved region II
F;168-178/Region: conserved region IV
F;231-252/Region: conserved region IV
F;231-248/Region: conserved region IV
F;231-248/Region: Li loop
F;241-252/Region: Location signal
F;241-252/Region: tetramer association
F;241-252/Region: tetramer association
F;241-252/Region: tetramer association
F;241-253,233/Alinding site: phosphate (Ser) (covalent) #status predicted
F;173-176,235,239/Alinding site: zinc (Cys, His, Cys, Cys) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-391 <LEA>
A;Cross-references: EMBL:X90592; NID:g1532043; PIDN:CAA62216.1; PID:g1532044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     timor suppressor p53 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Bate: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C;Accession: JC6193
R;Le Goas, E.; May, P.; Ronco, P.; de Fromentel, C.C.
Gene 185, 169-173, 1997
A;Title: CDNA cloning and immunological characterization of rabbit p53.
A;Reference number: JC6193; MUID:97208869; PMID:9055811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 LSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOSDISLELPLSQETFSGLWKLL------PPED----ILPSPHC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                           SQSTQTNEF-LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---MDDLLLPQ-----DVEEFFEGPSEALRVSGAPAAQDPVTETPGPVA-----
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                                                                                                                                                                                                                                                                                                                Length 381;
                                                                                                                                                                                                                                                                                                              29.5%; Score 702; DB 2; Length 38:
40.4%; Pred. No. 1.3e-46;
Live 58; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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40.7%; Pred. No. 2.1e-46;
tive 59; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|:: | | ::||; :|| ::||| PQKKKPLDGEYFTLKIRGRKRFEMFRELNEALEL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 IKKRRSPDDELLYLPVRGRETYEMLLKIKESLEL 384
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A;Gene: p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: tumor
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 40.4%
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Si
Matches 156,
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C2)Gotdes. Mus musculus (house mouse)
C; Species. Mus musculus (house mouse)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Accession: S38824 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Accession: S38824 #sequence_revision 13-Jan-1995 #text_change C; Accession: S38824 #sequence_revision 13-Jan-1995 #sequence rumber: S38824 #sequence rumber: S38825 #volecules generated by alternative splicing.
A; Reference number: S38824 #voles #sequence rumber: S38824 #volecule type: mRNA
A; Residues: 1-381 < ARA
A; Residues: S35478 #volecule type: mRNA
A; Residues: 1-381 < ARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVR 367
                                                                                                                                                                                                                                                                                                                                                            86
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                                                                                                                                                                                                                   LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPM--
                                                                                                                                                                                                                                              LSQETFSDLWKLL-----PPNNVLSTLPSSDS-----IEELFLSENVTG
                                                                                                                                                                                                                                                                                                              WPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIP
                                                                                                                                                                                                                                                                                                                                           SNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIR
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                                                                                                                                                                       Gaps
                                                                                                                                                                       90;
                                                                                                                          Length 393;
                                                                                                                   tch 29.5%; Score 704; DB 2; Length 39 al Similarity 38.6%; Pred. No. 9.3e-47; 165; Conservative 69; Mismatches 134; Indels
                                                      p53
                                                      tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---KREGP 390
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                             A;Gene: p53
C;Superfamily: cellular 1
C;Keywords: liver; tumor
                                                                                                                     Query Match
Best Local S:
Matches 165
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                                                                                                                                                                                                                                                                                                           69
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       C;Genetics;
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٥	71 OVTNI GIJINGMPOOTONGGGGGFGDVMPNHAONGVFADGDVAODGGFFDAT -GDGDA 125	A. Descrimental course, oftenin 100 cur
7		C, Genetics
qq	49VANWINEDPEEGIRVPAAPAPEA-PAPAAPALAAPATSWP 89	A;Map position: 9F1 A:Introns: 72/2: 208/3: 505/3: 675/3: 2889/3: 3582/1: 3851/3: 3886/1: 3930/1
ΟŊ	TYSTE	11/0000 10/11/00 11/200
qq		C;Function: A;Description: may be involved in cytomatrix organization at the site of neurotransmi
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ÿ 7		,
άα	150 PGTRVRAMAIYKKSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRAEYLDDRN 207	Query Match 4.8%; Score 114.5; DB 2; Length 3942; Rest Tocal Similarity 21.2%; Dred No 9.4.
δλ	242 TGRQSVLVPYEPPQVGTEFTTVLXVFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCF 301	les 113; Conservative 61; Mismatc
qq	208 TFRHSVVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTITILEDSSGNLLGRNSF 267	QY 1 MSQSTQTNPFLSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSED 44
Qy	302 EARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDEL 361	Db 2038 LGQGLQYGSFTDLRHPTDLLSHPLPLRRYSSVSNIYSDHRYGPRGDAVGFQEASLAQ 2094
QQ		Qy 45 -GATUKIEISMDCIRMQDSDLSDPWWPQYTNLGLLNSMDQQ-1QNGSSSTSPYNTD 98
٥		
· 42		ENDARMOODOO OO TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
}		
RESULT		
146226 Cellul	; ar tumor antigen o53 - dog (fragment)	QY 153WTYSTELKKLYCQIAKTCPLQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVK 203
C; Spec	ites: Canis lupus familiaris (dog)	Db 2192 VRAADGMIXSTINTPLAATLPITTQPASVLRPWVRGGMYRPYVSGGVT 2239
C; Date	:: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000. ssion: T46226	Negatian Manager 1906
R; Devi	lee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, C.	
Antica A:Titl	incer Res. 14, 2039-2046, 1994 e: The canine b53 gene is subject to somatic mutations in thymoid carcinoma	Db 2240 AVPLTSLTRVPMIAPRVPLGPAGLYRYPAPRFPIASSVPPAEGPVYLG 2287
A; Refe	rence number: 146226; MUID:95150524; PMID:7847847	Qy 258 TEFTTVLXNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACPG 310
A; Acce A; Stati	A;Accession: 146226 A;Status: preliminary; translated from GB/EMBL/DDBJ	: : Db 2288 KPAATKASGAGGPRPELPAGVAREEPFSTTAPAVIKEADVAPAPGPAPAPPP 2340
A; Mole	cule type: DNA	
A; Resi	.dues: 1-77 , <dev> .s-references: GB:L27630: NTD:a508454: PTDN:AAC37327.1: PTD:a508455</dev>	Qy 311
C; Gene	tics:	Db 2341 GQKPAGEAAAGSGSGVLSRPASEKEEASQEDRQRKQQEQ 2379
A; Intro	: p33 ons: 24/1; 61/3	OV 348 MTSIKKRRSPDDELLYLPVRGRETYEMLIKIKESLEIMOYLPOHTIET 395
C; Supe	C;Superfamily: cellular tumor antigen p53	
Quer		מינים במקנים במק
Best Lo Matches	<pre>cal Similarity 60.3%; 47; Conservative 10</pre>	OY 396 YRQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
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3 1		
QQ	1 KSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAKYLDDRYTFRHSVVVPYEP 59	RESULT 15
٥y	254 PQVGTEFTTVLXNFMCNS 271	132008 hypothetical protein K10G6.3 - Caenorhabditis elegans
qq		C;Species: Caenorhabditis elegans C.Date: 20-Ort-1000 #eamenra ravision 20-Ort-1000 #text change 20-Ort-1000
!		C; Accession: T32008
RESULT 14	. 14	R;Davidson, S.; Wohldmann, P.; Mullen, G. submitted to the EMBL Data Library, July 1997
T42730		A; Description: The sequence of C. elegans cosmid K10G6.
C; Spec	bassoon procein - mouse C.Species: Mus musculus (house mouse)	A; Reference number: 221111 A; Accession: T32008
C; Date	:: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000 ssion: ¶42730	A; Status: preliminary; translated from GB/EMBL/DDBJ
R, Diec	R;Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex,	
A;Titl	J. Cell Biol. 142, 499-509, 1998 A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized	 A;Cross-references: EMBL:AF016669; PIDN:AAB66098.1; GSPDB:GN00020; CESP:K1066.3 A;Experimental source: strain Bristol N2; clone K1066
A; Refe A; Acce	A;Reference number: Z22249; MUID:98345363; PMID:9679147 A;Accession: T42730	C;Genetics: A;Gene: CESP:K10G6.3
A;Stat A;Mole	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	A;Map position: 2 A;Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3
A; Resi	A;Residues: 1•3942 <die> A:Cross-references: EMBL:V17034: NTD:g3413809: PIDN:GAA76598.1: PID:g3413810</die>	Ouerw Watch 4 7%: Score 111 5: DB 2: Length 1819:
		4:/4; SCOIE III:3; DB 2;

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N:AAB66098.1; GSPDB:GN00020; CESP:K10G6.3
N2; clone.K10G6
                                                                                                                   29-Oct-1999 #text_change 29-Oct-1999
1645/2; 1700/2; 1768/1; 1797/3
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15;	140	803	200	862	246	920	300	096	345	1020	403	1056	,	
Gaps	PHSFDV	TATV	AEHVTE	MDQQIQ	ITGROS	IRQP	VLGRRC	RRS	RQNTHG	PLONPHN	0000	ONITONO	•	
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153;	STFDAL	, JAPQPĽ	KVMTPP	EASSSM		QUPPQ	RPILI	HKNTDLVLIT	FRKOOV) PVAYOV	SELELM	NVYQQV(32
19.4%; Pred. No. 5.4; ttive 65; Mismatches	QIQNGSSSTSPYNTDHAQNS VTAP - SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDV	KVAASSSSNSAASRPPSQPSTPATAPATPMLQASQAPQPLQAPPQSPMET	SFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTE	TYTKTTVPPSVANTWNTEKAQLISPKPRSQTIFSEASSSMTVGDALRAQQHQQKMDQQIQ	601	I : : : : : : : : : : : : : : :	VLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLFTRDGQVLGRRC 300		CPGRDRKADEDSIRKOOVSDSTKNGDGTKRPFRONTHG	961 SEGLVAVTSTPLPPIQLPQRSQAPAPSRQQQQPPVAYQVQFNGRPLPPMQLPPLQNPHN 1020	IQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQ	1056	HQHLLQKHLLSACFRNELVEPRRETPKQSDV 434	HHHQQQHHQQNQQQAPGNRSRSHSNV 1082
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Search completed: August 7, 2003, 09:53:26 Job time: 18.1241 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 7, 2003, 09:32:13; Search time 7.94483 Seconds (without alignments) 2651.784 Million cell updates/sec Run on:

US-09-538-106-15 2383 1 MSQSTQTNEFLSPEVFQHIW......PRQSDVFFRHSRPPNRSVXP 448 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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PCLO_HUMAN FTFB_DROME PKSM_BACSU PTPD_HUMAN	FXN3_HUMAN SDC_DROME	SFL1_YEAST SNF2_YEAST SIMA_DROME	Y586_HUMAN
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ALIGNMENTS

ALLONMENTS	SULT 1 3_HUMAN P73_HUMAN	AC	15-SEP-2003 (Rel. Tumor protein p73	protein). TP73 OR P73.	Homo sapiens (Human). Eukaryota; Metazoa; Chordata;	OC Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID-9606; bn 111	KN F1. RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA). RC TYTSGIFF-CAJON	MEDLINE=97433090; PubMed=9288759;	RA Kaghad M., Bonnet H., Yang A., Creancier L., Biscan JC., Valent A., RA Minty A., Chalon P., Lelias JM., Dumont X., Ferrara P., McKeon F.,	ically expressed dene related to n53 at 1n36 a region	Tracementaries of the control of the	RP SEQUENCE FROM N.A. (ISOFORM ALPHA). RX MEDITNE-99289209: PubMed=10362363:	RA Harris C.C.; RT "Mutational analysis of p73 and p53 in human cancer cell lines.":	Oncogene 18:3415-3421(1999).	RN [3] RP SEQUENCE FROM N.A. (ISOFORM ALPHA).	MEDLINE=98389621; PubMed=9721206;	KA Mai M, Huang H., Keed C., Qian C., Smith J.S., Alderete B., ba Jankine b cmith D T Tim E.	oligodenc	-	RP SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).	MEDLINE=99021697; Pubmed=9802988;	RA De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,		RL J. Exp. Med. 188:1763-1768(1998). RN [5]	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETP		RA COStanzo A., Levrero M., Knight R.A.; RT "Additional complexity in p73: induction by mitogens in lymphoid cells	
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     DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRAST TO PS3. HEMIZYGOSITY IS OBSERVED IN NEUROBLASTOMA AND OLIGODENDROGLIOMA. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.
                                                                                    MEDLINE-99318135; PubMed-10391251;
Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
Kharbanda S., Weichselbaum R., Kufe D.;
"p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
to DNA damage.";
Nature 399:814-817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN.

SUBBUIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABLIVED TO THE ABLIVED TO THE ABLIVED TIME TIME C-TERMINAL SOFFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA SUBCELLULAR LOCATION: Nuclear.

ALTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORM DELTA SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOId-015350-7; Sequence-VSP_006538; ISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER, SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS. INDUCTION: NOT INDUCED BY DNA DAMAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isold-015550-3; Sequence-VSP_006540, VSP_006541;
Note-The splicing of exon 11 results in a frameshift from the original reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Epsilon;
Isoid=015350-5; Sequence=VSP_006544, VSP_006545;
Note=The splicing of exon 11 results in a frameshift from the
original reading frame. The splicing of exon 13 reverts the
reading frame to the sequence of isoform Alpha;
                                                                                                                                                                                                                                                                                                           MEDLINE-99380160; PubMed=10449409;
Chi S.W., Apred A., Arrowsmith C.H.;
Chi S.W., Apred A., Arrowsmith C.H.;
Chi S.W., Abrowsmith C.H.;
Eshlution structure of a conserved C-terminal domain of p73 with structural homology to the SAM domain.";
EMBO J. 18:4438-445(1999).
-I- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
WHEN OVERRENDUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
                                                                                                                                                                                          Ή.
                                                                                                                                                                                     Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu
Kharbanda S., Weichselbaum R., Kufe D.;
Nature 400:792-792(1999).
                                       Thomas D.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=015350-4; Sequence=VSP_006542, VSP_006543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event-Alternative splicing; Named isoforms=7;
                                                                           PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
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IsoId=015350-2; Sequence=VSP_006539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=015350-1; Sequence=Displayed;
                                                                                                                                                                                                                                                             Kaelin W.G. Jr.;
"The emerging p53 gene family.";
J. Natl. Cancer Inst. 91:594-598(1999).
Cell Death Differ. 6:389-390(1999).
                            SEQUENCE FROM N.A. (ISOFORM KAPPA).
                                                                                                                                                                                                                                                   MEDLINE-99217940; PubMed-10203277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPE
CYRMITWREADDLKQGPUSTRAQGLRSSNRATISIGGSGE
LQRQRVMEAVHFRYRHTITPNRGCPGGGDDGWAFFEDLP
DCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
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ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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MIM; 601990; -.
60; 60:0003700; F:transcription factor activity; TAS.
60; 60:0006630; P:induction of apoptosis by DNA damage; TAS.
60; 60:0006298; P:induction of apoptosis by DNA damage; TAS.
10terPro; IPR002117; P53.
10terPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
Pfam; PF00870; SAM: 1.
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                                                                          48
                                                     23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE. WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN
                                                                                                                                           MDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP
                                                                                                               IKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELGRDFNEGOSAPASHLIRVEGNNL
                                                                                                                                                                                                                                      AQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDG
                                                                                                                                                                                                                                                  QVLGRRCFEARICACPGRDRKADEDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--T
                                                                                                                                                                                                                                                                                              SIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQ--QQHQHL
                                                                                                                                                                                                                                                                                                                                         343 GVKKRRHGDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                     ---EIS
                                                                                                                                                                                           IKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSH
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL TYROSTHE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                          P73_CERAE STANDARD; PRT; 637 AA.
095XSR6; 09TSOB;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor protein P73 (p53-like transcription factor) (p53-related protein).
                                                     1 MSQSTQTNEFLSPE---VFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKI-
                                31;
         636;
         Length
                                84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caput D.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                      Score 1297.5; DB 1;
Pred. No. 8.7e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA)
        54.4%; Score 1297.5;
61.4%; Pred. No. 8.7e
                               47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=09XSK8-2; Sequence=VSP_006537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9XSK8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Cercopithecus.
NCBI_TaxID-9534;
                               258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name-Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name-Beta;
                                                                                                54
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         Query Match
                     Best Local
                               Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BRBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                           Probom; PD002681; F55; 1.

PROSTIE; PS00348; P55; 1.

PROSTIE; PS00348; P55; 1.

Transcription regulation; Activator; DNA-binding; Anti-oncoye...,
Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
SFLTGLGCPNCIEYFTSOGLOSIYHLQNLTIEDLGALKIPE OYARSPLIC 495 637 SFLTGLGCPNCIEYFTSOGLOSIYHLQNLTIEDLGSG ELORORNWEAVHFRVRHTTIPNRGGPGSDEWADFGFDL PDCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 MDVFHLEGMTTS-----VMAQFNLLSSTMDQMSSRAASASPYTPEHAA-SVPTHSPYAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 MDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 IKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQYVEDPITGRQSVLVPYEPPQVGTEFTTVLXNFMCNSSCVGGMNRRPILIIVTLETRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 QVLGRRCFEARICACPGRDRKADEDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 SIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQ---QQHQHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 GVKKRRHGDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSQSTQTNEFLSPE---VFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKI----EIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAQSTTT----SPDGGTTFEHLWSSLEP------DSTYFDLPQSSRGNNEVVGGTDSS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular tumor antigen p53 (Tumor suppressor p53).
TP53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1296.5; DI
Pred. No. 1e-88;
48; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366
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                                                                                                                                                                                                                                                                                                                                  PRINTS: PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.4%;
                                                                                                                                                                           EMBL; Y11419; CAA72224.1; -. EMBL; Y11419; CAA72225.1; -. HSSP; O15350; 1COK.
                                                                                                                                                                                                                                                                       SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 61.2 es 257; Conservative
                                                                                                                                                                                                                                             InterPro; IPR002117; P53
InterPro; IPR001660; SAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                        Pfam; PF00870; P53; 1.
Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P53_ONCMY P25035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103
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Matches
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P53_ONCMY
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us-09-538-106-15.rsp

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P53_BARBU
               267
                                        361
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SEQUENCE
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                                                                                                                                                Q9W678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                         RESULT 4
P53_BARBU
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                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDALS-PSPAIPS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 NTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 VPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICAC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGRDRKADEDSIRKQQ----VSDSTKNGDGTKRPFRQ-NTHGIQMTSIKKRRS----PDDE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39
                                                                        de Fromentel C.C., Padkel F., Chapus A., Baney C., May P., Soussi T., Rainbow trout p53: cDNA cloning and blochemical characterization."; Gene 112:241-245(1992).

19. FONCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BCI-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 GYDNF----MMEAPLQ-----VEFDPSLFEVSATEPAPQPSISTLDTGSPPTSTVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KMNLNLVAVQPPETE----SWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 MPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Phosphorylation; Apoptosis,
DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY SIMILARITY).
8422250765545AlC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 396;
             Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                      expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Mismatches 102; Indels
 Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 847.5; DB 1
Pred. No. 1.1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
OLIGOMERIZATION.
                                                 SEQUENCE FROM N.A. MEDLINE=92210006; PubMed=1339362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43966 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 LSQESFEDLW------
Actinopterygii; Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M75145; AAA49605.1; -. PIR; JH0631; JH0631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PIR; JH0631; JH0631.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325
369
303
395
395
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                         NCBI_TaxID=8022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA_BIND
DOMAIN
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MOD_RES
SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
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84 QIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 ELINDEYLPSSFDDNIFDNVLTEQPQPSTSP-----PTASVPVATDYPGEHGFKLGF 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barbus barbus (Barbel).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophys1; Cypriniformes;
Cyprinidae; Barbus.
NCBI_TaxID=40830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein; Phosphorylation; Apoptosis.

DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
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                                                                                                                                                                                                       : | :||:| |||| | :||| : || : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : || : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : || : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : || : || : ||| : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-UCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
TP53 OR P53.
                                                                                                                                           LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Pfam; PF00870; P53; 1.
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Best Local Similarity 51.28
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40,
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298
342
276
368
369 AA;
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us-09-538-106-15.rsp

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P53_ICTPU
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                         262
                                                             195
                                                                                 322
                                                                                                                          373
 202
                    137
                                                                                                                                      DQ---ETKTLDKIPSANKRSLTKDSTSSVPRPEGSKKAKLSGSSDEEIYTLQVRGKERYE 312
QQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVV
          KRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTT
                                                   VLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRK
                                                                                           QQVSDSTKNGD----GTKRPF-RQNTHGIQMTSIKKRR----SPDDELLYLPVRGRETYE
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-97344388; Pubmed-9200835;
Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
Thongtan T., Bantes D.W., Hendricks J.D., Bailey G.S.;
"Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota: Metazoa: Chordata: Cranlata; Vertebrata; Buteleostomi;
Actinopterygil; Neopterygil; Teleostel; Ostariophys1; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                         P53_BRARE STANDARD; PRT; 373 AA. P79734; Q90440; Col.NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor p53). TP53 OR DRP53.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Mar. Biol. Biotechnol. 6:88-97(1997)
                                                                                                                                                                 374 MLLKIKESLELMQYLPQHTIETYRQQ 399
                                                                                                                                                                             embryoqenesis.
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InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 140-212 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U60804; AAB40617.1;
EMBL; U46693; AAA97408.1;
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                   expression during
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143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Luft J.C., Bengten E., Clean L.W., Miller N.W., Wilson M.R.;
Luft J.C., Bengten E., Clean L.W., Miller N.W., Wilson M.R.;

"Identification and characterization of the tumor suppressor p53 in channel catfish (Irctalurus punctatus).";

Comp. Biochem. Physiol. 1208:675-682(1998).

-I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                          112 QPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGQVLGRRCFEARICACPGRDRKADEDSIRK-QQVSDSTKNGDGTKRPFRQNTHGIQM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                    BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                      Nuclear protein; Phosphorylation; Apoptosis.
1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ
                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY SIMILARITY). AC7AB724FA6B61FF CRC64;
                                                                                                                                                                                                                                                                                                                                          33.8%; Score 805.5; DB 1; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression (By similarity).
-!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                          Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                   1.3e - 52
                                                                                                                                                                                               OLIGOMERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     42;
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P535UPPRESSR.
ProDom; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                          41899 MW;
                                                                                                                                                                                                                                                                                                                                                                 53.9%;
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366
296
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                                                                                                                                                                                                                                                                                          373 AA;
                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          158;
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093379;
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                                                                                                                                                                    DNA_BIND
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Sest Local
Matches 15
                                                                                                                                                                                                                                                                      MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 SDMLQPQSS--SSPPTSTVPVTSDYPGLLNFTLHFQESSGTKSVTCTYSPDLNKLFCQLA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHL 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 ASKKSKNSSSDDEIYTLQVRGKERYEFLKKINDGLELSDVVPPADQEKYRQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPYAOPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 KTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR
                                                                                                                                                                                                                                                                                                                                           BASIC (REPRESSION OF DNA-BINDING).
WUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
1B89CD98DB3289F2 CRC64;
                                                                                                                                                      HSSP; r. IPR00411., r. Interpro; IPR00411., r. Pfam; PF00870; P53; 1. R. PRINTS; PR00386; P53SUPPRESSR. R. ProDom; P0002681; P53; 1. Brocom; P0002681; P53; 1. BrostTe; P800348; P53; 1. BrostTe; P800348; P53; 1. RANSCRIPTION ACTIVATION; Activator; KW Anti-oncogene; DNN-binding; Transcription activator; KW Nuclear protein; Phosphorylation; Apoptosis. r. Andin 1 36 BY SIMILARITY. OLIGOMERIZATION. OLIGOMERIZATION. OLIGOMERIZATION. OLIGOMERIZATION. C. REPRESSION OF DNA-BINDING).
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Soussi T., de Fromentel C.C., Mechali M., May P., Kress M.;
"Cloning and characterization of a cDNA from Xenopus laevis coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 1; Length 376; 3.5e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 3.5e
45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 ----LLSKTCRKERDGAAGEPKR 362
                                                                                                                                        EMBL; AF074967; AAC26824.1; -. HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                               41989 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               33.6%;
50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                             376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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SEQUENCE FROM N.A.
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P07193;
                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 DALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVM 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTF 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
T -> S (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                            2 SQSTQTNEFLSPEVFQHIWDFLEQPI----CSVQPIDLNFVDEPSEDGATNKIEISMDCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SSETGMDPPLSQETFEDLWSLLPDPLQTVTCRLDNLS-EFPDYP------LAADMT
                                                        Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.; "Overexpression of Wild-type p53 interferes with normal development in Xenopus laevis embryos."; Oncogene 9:109-120(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein; Phosphorylation; Apoptosis.

1 29 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CE1F3E58F020D74D CRC64;
protein homologous to human and murine p53.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.6%; Score 777.5; DB 1; 42.5%; Pred. No. 1.5e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 VLQE------GLMGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Mismatches
                                     SEQUENCE FROM N.A. MEDLINE-94134403; PubMed=8302570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P535UPPRESSR.
Probom; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40692 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X05191; CAA28821.1; -.
EMBL; X77546; CAA54672.1; -.
EMBL; S68353; AAC60746.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M36962; AAA49923.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 42.5
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A29376; A29376.
HSSP; P04637; 1TUP.
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71
296
363 AA;
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DOMAIN
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CONFLICT
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expression
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P41685;
                Query Match
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                            297
                                                                                               242 RRCFEVRVCACPGRDRRTEEDNYTKKRGLKPSGK------RELAHPPSSEPPLPKKR 292
SPPPRGSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
"Evolutionary conservancy of p53 gene sequences in fish.";
"Evolutionary conservancy of p53 gene sequences in fish.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle. Fegulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                         RRCFEARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKR
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OLIGOMERIZATION.

BASIC (REPRESSION OF DNA-BINDING).

BUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

PHOSPHORYLATION (BY SIMILARITY).

ACCIOEE22F5F9CFD CRC64;
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
extinopterygli; Neopterygli; Taleostel; Euteleostel; Neoteleostel;
Acanthomorpha; Acanthopterygli; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein; Phosphorylation; Apoptosis.

1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                         R---SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 393
                                                                                                                                                                   293 LVVVDDDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV 334
                                                                                                                                                                                                                                                                                                          Cellular tumor antigen p53 (Tumor suppressor p53).
TP53 OR P53.
                                                                                                                                                                                                                                                               70.007-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                         367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                         Tetraodon miurus (Congo puffer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF071571; AAD34213.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
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PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002117; P53.
                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308
342
288
366
367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=94908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P04637
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09W679;
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SEQUENCE
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249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS-----PDDELLY 363
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                                                                                                                                                                                                                                                                                                          41
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                                                                                                                                                                                                          11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 AERQMNAMCNFMDSTFNEALFNLLP-------EPPSRDGANSSSPTVPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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J. Vet. Med. Sci. 55:801-805(1993).
J. Vet. 
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                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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MEDLINE-94114699; PubMed-8286534;
Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T., Goitsuka O'Riien S.J., Tsujimoto H., Hasegawa A.;
"Molecular cloning and chromosomal mapping of feline p53 tumor
                                                                                                     64;
     DB 1; Length 367;
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
08-FBE-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
TP53 OR TRP53.
                                                                                                     53; Mismatches 105;
32.6%; Score 776; DB 1
42.6%; Pred. No. 2e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 LPVRGRETYEMLLKIKESLELMOYLPO 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :|||: |||| ||: |:|:: |:
313 LOIRGRKRYEMLKKINDGLDELENKPK 339
                                                                                                                                                                                                                                                                          || : || :|| :|
10 LSQDTFQDLWDNVSAP----PIS----
                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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MEDLINE=94333960; PubMed=8056458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Int. J. Cancer 58:602-607(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Felis silvestris catus (Cat).
                                                                                                     Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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MOD_RES
SEQUENCE
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                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       .7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSFVPSQKTYPGAYGFHLGFLQSGTAKSVTCTYSPPDLNKLFCQLAKTCPVQLWVRSPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 FRHSVVVPYEPPEVGSDCTIHYNFMCNSSCMGGMNRRPIITITLEDSNGKLLGRNSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VANWLDEA-----PDDASGMSAVPAPAAPAPAT-----PAPAISWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT
                                                                                                                                                                                                                                                                                                                     BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
         SUBCELLULAR LOCATION: Nuclear. DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                 Transcription regulation; Activator;
                                                                                                                                                                                                                                                                          Nuclear protein; Phosphorylation; Apoptosis.
DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                               Score 770; DB 1; Length 386; Pred. No. 6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Mismatches 103; Indels
 SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSQETFSELWNLLPE------NNVLSSELSSAMNELPLSED---
                                                                                                                                                                                                                                                                                                                                                                                -> R (IN REF. 2).
D08B43BA1BC8EB78 CRC64;
                                              in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                            OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 TLQIRGRERFEMFRELNEALEL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 YLPVRGRETYEMLLKIKESLEL 384
                                                                                                                                                                                                                                                                                                                                                                                           42692 MW;
                                                                                                                                                                                                                              PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                     EMBL; D26608; BAA05653.1; -. EMBL; D16460; BAA03927.1; -. HSSP; P04637; 10LG.
                                                                                                                                                                                                                                                              Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                  32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                          42.18;
                                                                                                                                                                                                      InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                      ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                   385
285
386 AA;
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DNA_BIND
DOMAIN
DOMAIN
MOD_RES
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CONFLICT
SEQUENCE
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P53_PIG
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386 AA.

PRT;

STANDARD;

P53_PIG Q9TUB2;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70
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                                                                                                                                                                                                                                                                                MEDLINE-99422034; PubMed-10490836; Burr P.D., Argyle D.J. Reid S.W.J., Nasir L.; "Nucleotide sequence of the porcine p53 cDNA, and the detection of recombinant porcine p53 expressed in vitro with a variety of anti-p53 antibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                                    -----VTNWLDENPDDASRVPAP-----PAATAPAPAPAPATSWPL--SSFVPSQK
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PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBUNIT: Binds DNA as a homotetramer (By similarity).
-i- SUBCELLULAR LOCATION: Nuclear.
-i- DISEARS: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.
-i- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                               Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein; Phosphorylation; Apoptosis. J
DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
DINA BIND 91 BY SIMILARITY.
DOMAIN 318 349 OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY SIMILARITY).
A4C3D88E8DF55162 CRC64;
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                                                                                                                              Sus scrofa (P1g).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutherla; Cetartiodactyla; Suina; Suldae;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.2%; Score 767; DB 1
38.6%; Pred. No. 1e-49;
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ProDom; PD002681; P53; 2.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF098067; AAF04620.1; -. HSSP; P04637; 1C26.
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42862 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002117; P53.
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Best Local Similarity 38.6
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380
316
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression.
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361
304
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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                                                 DOMAIN
DNA_BIND
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Best Local S
Matches 169
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                                                                                                             MOD_RES
SEQUENCE
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                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
272
                                                                                                                                                    VYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVP 250
                                                  YEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACPG 310
                                                                                                                                     RDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 16:11383-11383(1988).

- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bol-2 expression (By similarity).

- SUBBUILT: Blids DMA, as a homotetramer (By similarity).
                                                                                                   213 YEPPEVGSDCTTIHYNFMCNSSCMGGMNRRPILTITLEDASGNLLGRNSFEVRVCACPG
                                                                                                                                                                                     371 TYEMLLKIKESLELMQYLPQHTIETYRQ--QQQQQHQHLLQKHLLSACFRNELVEPRRET
                                                                                                                                                                                                          330 RFEMFRELNDALELKD------KGQS
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauría; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear
                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89083584; PubMed-3060861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                          PS-----RHKKP 376
                                                                                                                                                                                                                                   429 PKQSDVFFRHSKP 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X13057; CAA31456.1;
                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00870; P53; 1
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HSSP; P04637; 1TUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oncoprotein.
                                                                                                                                                                                                                                                                                                                       P53_CHICK
P10360;
                                                                                     251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 EDYGGDFDFRVGFVEAGTAKSVTCTYSPVLNKVYCRLAKPCPVQVRVGVAPPPGSSLRAV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRDRKADEDSIRKQQVSDSTKNGDG--TKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVR 367
                                                                                                                                                                                                                                                                                                                                                                                             69
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Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
Watari T., Hasagawa A., Tsujimoto H.;
"Aberrations of p53 tumor suppressor gene in various spontaneous
tumors in the dog.";
                                                                                                                                                                                                                                                                                                                                                                                                                             9 TEPTEVEMDLWSMLPY---SMQQL-----PLPEDHSNWQELS----PLEPSDPPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AVYKKSEHVAEVVRRCPHHERCGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
                                                                                                                                                                                                                                                                                                                                                                                             LSP-EVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 PPPLPL-----TPPRAAPSPVVPST
                                                                                                                                                              BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSHHORYLATION (BY SIMILARITY).
FC37D0FCDF9195B6 CRC64;
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Veldhoen N., Milner J.;
Isolation of canine p53 cDNA and detailed characterization of the
full length canine p53 protein.";
Oncogene 16:1077-1084(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                          Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                              55;
PROGUTE: PS00348; P53; 1.
Anti-oncogene; DNA-binding; Transcription regulation; Activator Anti-oncogene; DNA-binding; Transcription regulation; Activator Nuclear protein; Phosphorylation; Apoptosis.

TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                            DB 1; Length 367;
                                                                                                                                                                                                                                                                                         32.1%; Score 764.5; DB 1; Length 3 44.6%; Pred. No. 1.4e-49; ive 50; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                              BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 AA
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MEDLINE=98178696; Pubmed=9519881;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P53_CANFA STANDARD; 1029537; 09TV78; 01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                          40169 MW;
                                                                                                                                                                                                                                                                                                                    cal Similarity 44.69
169; Conservative
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292
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367, AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 KTYPGTYGFRIGFLHSGTAKSVTWTYSPLINKLFCQLAKTCPVQLWVSSPPPPNTCVRAM 147
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                                                                                 Kraegel S.A., Pazzi, K.A., Madewell B.R.;
"Sequence analysis of canine p53 in the region of exons 3-8.";
"Sequence analysis of canine p53 in the region of exons 3-8.";
"Sequence analysis of canine p53 in the region of exons 3-8.";
"Sequence analysis of canine p53 in the region of exons 3-8.";
"It is a set or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSD-PMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 LSQETFSELWNLLPE------NNVLSSELCPAVDELLLPESVVNWLDEDSDDAPRM
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                                                                                                                                                                                                                                                                                                                                               DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.

LIGOMERIZATION.

BASIC (REPRESSION OF DNA-BINDING)

NUCLEAR LOCALIZATION SIGNAL (POTE)
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PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.6%; Score 753.5; DB 1; Length 381;
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                                                                                                                                                                                                                                                                                                              SUBUNIT: Binds DNA as a homotetramer (By similarity).
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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L -> P (IN REF. 2).
761A718FDC93DA59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear.
                                                                      MEDLINE=95323915; PubMed=7600529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF060514; AAC16909.1; -.
EMBL; AB020761; BAA78379.1; -.
FWRT: S77819; AAB42022.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00870; P53; 1.
PRINKIS, PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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HSSP; P04637; 10LG.
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375
311
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356
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MOD_RES
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148 AIYKKSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAKYLDDRNTFRHSVVV 206
                                                                                                                                            310 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;

"Isolation of CDNAs encoding the p53 tumor suppressor gene in the
"Isolation of CDNAs encoding the p53 tumor suppressor gene in the
Japanese Medaka (Orylas latipes).";

Submitted (MAX-1997) to the EMBL/GenBank/DDBJ databases.

-I FUNCTION: Acts as a tumor suppressor in many tumor types;

growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes regulared for this process. One of
the activated genes is an inhibitor of cyclin dependent kinases.

Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
MEDLINE-97305153; PubMed-9161419;
Krause M.K., Rhodes L.D., van Beneden R.J.;
Kloning of the p53 tumor suppressor gene from the Japanese medaka (Oryzias latipes) and evaluation of mutational hotspots in MNNG-exposed fish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryzlas latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Actinopterygli; Neopterygli; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygli; Percomorpha; Atherlnomorpha;
Beloniformes; Adrianichthyldae; Oryzlinae; Oryzlas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P53_ORYLA STANDARD; PRT; 352 AA. P79820; 09PSU7; 09PSU8; 01-NOV-1997 (Rel. 35, Created) 28-FFB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANT THR-91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF003949; AAD01195.1; -. AF003950; AAD01196.1; -.
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EMBL; AF003949; AAD01195.1: -
                                                                                                                                                                                                                                       324 ERYEMFRNLNEALEL 338
                                                                                                                                                                                                 ETYEMLLKIKESLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002117; P53.
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Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TP53 OR P53.
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                                                                                                                                                                                                                                                                                                                                                                                                                        311
                                                                                                                                                                                                                                                                           136 HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKA 195
                                                                                                                                                                                                                                                                                       256 VGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKA 315
                                                                                                                                                                                                                                                                                                                                                                      1:1 | 1:1 | 1:1|| | 1|| | 1|| | 1|| | 1:1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 265
207 PGSEMTILLSYMCNSSCMGGMNRRPILTILLITLET-EGLVLGRRCFEVRICACPGRDRKT 265
                                                                                                                                                                                                                                  76 GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGP 135
                                                                                                                                                                                                                                                                                                                     EHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQ 255
                                                                                                                                                                                                                                                                                                                                                                                                    DEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS------PDDELLYLPVRG 368
                                                                                                                                                                                                                52
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                                                                                                                                                                                                                                                                                                                              FQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPQYTNL
                                                                                                                                                                                                             14 FOELWETVSYP--PLETLSLPTVNEPTGSW-----VATGDMFLLDQDLS-----
                                                                                                                                                                                                                                                      ---GTFDDKI-----FDIP---IEPVPINEVNPPPTTVPVTTDYPGS
                                                                                        NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                               Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F., Kettmann R., Burny A., Willems L.; ide sequence of the bovine P53 tumor-suppressor cDNA.";
                                       Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.

J 48 TRANSCRIPTION ACTIVATION (ACIDIC).

DNA_BIND 87 273 BY SIMILARITY.
                                                                                                                                                                          69
                                                                               BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTEN
                                                                                                                                                     DB 1; Length 352;
                                                                                                                                                                          Indels
                                                                                                                      MISSING (IN REF. 1).
196868A66351BFF5 CRC64;
                                                                                                                                                                         92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Bovine; STRAIN-Holstein; TISSUE-Thymus;
                                                                                                                                                               3e-48;
                                                            BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 AA
                                                                                                                                                                         54; Mismatches
                                                                                                                                                    31.3%; Score 746.5; 43.1%; Pred. No. 3e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE-95352829; PubMed-7626789;
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RERYEFLKKINDGLELLE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                          RETYEMLLKIKESLELMQ 386
                                                                                                                                 MW.
 PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 13-386 FROM N.A.
                            Anti-oncogene; DNA-binding;
                                                                                                                       22
39753 1
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq. 5:261-264(1995).
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          PD002681; P53; 1
PS00348; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                     331
350
295
351
91
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NCBI_TaxID=9913, 9915;
                                                                             334
283
351
91
22
352 AA;
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  indicus (Zebu)
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide
                                                                                                                                                               Best Local Sim
Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P53_BOVIN
Q29628;
                                                                                                                      CONFLICT
                                                                                                                                                                                            16
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                    PROSITE;
                                                                                                                                                     Query Match
 PRINTS;
                                                                                                   MOD_RES
                                                                    DOMAIN
DOMAIN
DOMAIN
                                                                                                               VARIANT
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P53_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                              Bishop R.R.P., Gobright E.E.I.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling as est of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BcI-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFVPSQKTYPGNYGFRLGFLQSGTAKSVTCTYSPSLNKLFCQLAKTCPVQLWVDSPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 OYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 LLPYTDVATWLDECPNEAPQMPEP-----SAPAAPPPAT----PAPATSWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
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LIGOMERIZATION
BASIC (REPRESSION OF DNA-BINDING).

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                            Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.;
"Predominant p53 mutations in enzootic bovine leukemic cell lines.";
Vet. Immunol. Immunopathol. 52:53-63(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBDUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
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222473F28C548F31 CRC64;
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                                                                                                                                                                              STRAIN-Boran; TISSUE-Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in many types of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY
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MEDLINE=96401400; PubMed=8807776;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00386; P535UPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
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                                                                                                                                                                              SPECIES-B.indicus;
                                                                                                                   [3]
SEQUENCE FROM N.A.
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DNA_BIND
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A Feltelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;

Partial characterization of the woodchuck tumor suppressor, p53, and its interaction with woodchuck hepatitis virus X antigen in hepatocarcinogenesis.";

Oncogene 15:327-336(1997).

Concogene 15:327-336(1997).
                                                                                              303 ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDEL 361
                                                                                                                                                                                                                                                              362 LYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQH-QHLLQKHLLS-ACFRN 419
                                                                                                                                                                                             243 GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Pfam; PF00870; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                           420 ELVEPRRETP 429
                                                                                                                                                                                                                                                                                                                                                                                                        376 PML--KREGP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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NCBI_TaxID=9995;
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036006;
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                                                                                                                                                                                                                                                                                                             11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                      71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                39 PMDDL-LLSSED--VENWFDK----GPDEALQMSAAPARAPTPAASTLAAPSPATSWPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNT-----HGIQMTSIKKRRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQHQHLLQKHLLSACF
                                                  BY SIMILARITY.
OLIGOMERIZATION.
OLIGOMERIZATION.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                   -----ENNALSPVLSP
                                                                                                                                                                                                                                                                      70; Gaps
Transcription regulation; Activator;
                Phosphorylation; Apoptosis. 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                      SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                               DB 1; Length 391;
                                                                                                                                                                                                                                                                      68; Mismatches 130; Indels
                                                                                                                                                                                         E1DE5DB84BA40182 CRC64;
                                                                                                                                                                                                                               30.9%; Score 736; DB 1
38.0%; Pred. No. 2e-47;
                                                                                                                                                                                                                                                                                                                                                 14 LSQETFSDLWNLLP------
                                                                                                                                                                                           43468 MW;
Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNELVEPRRETP 429
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RHKKIIFKREGP 388
                                                                                                                                                                                                                                                                      164; Conservative
                                                                         354
385
321
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                           391 AA;
                  Nuclear protein;
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                                                                                                                                                                                             SEQUENCE
                                                      DNA BIND
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Best Local
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DOMAIN
DOMAIN
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Search completed: August 7, 2003, 09:47:26 Job time: 9.94483 secs 099jd9 rattus norv 088899 mus musculu

075922 homo sapien

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August 7, 2003, 09:41:09; Search time 36.046 Seconds (without alignments) 3207.225 Million cell updates/sec
                                                                  US-09-538-106-15
2383
1 MSQSTQTNBFLSPEVFQHIW......PRQSDVFFRHSKPPNRSVYP 448
                                                                                                                          830525
     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                              protein search, using sw model
                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Maximum DB :
                              OM protein
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                                          Run on:
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Ogpib6 homo sapien Ogpib5 homo sapien Ogpib5 homo sapien Ogubv9 homo sapien Ogubv9 homo sapien Oggyd9 mus musculu Oggyd6 rattus norv Ogup74 homo sapien O75080 homo sapien Ogget2 mus musculu Oggyd6 brachydanio Oglib2 brachydanio Oglib2 mus musculu Ogwi64 barbus barb Oglip2 mus musculu Ogwi64 homo sapien Ogkyf6 homo sapien Ogkyf6 homo sapien Ogkyf6 homo sapien Ogkr06 homo sapien Ogkr06 homo sapien Ogkr06 homo sapien Ogskr06 mus musculu Ogskr06 homo sapien Ogskr06 mus musculu Ogskr06 homo sapien Ogskr06 mus musculu Ogskr06 mus musculu Ogskr06 mus musculu

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133333

ALIGNMENTS

Q8TDY5 Q8TDY6 Q96KR0 Q9CU77

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mc:*
sp_mc:*
sp_organele:*
sp_phage:*

sp_archea:*
sp_bacteria:*

SPTREMBL_23:*

Database

RESULT 1		_		DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)	DR TA D63 gamma (P51 isoform TAP63GAMMA)		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OX NCBI_TaxID=9606;		RP SEQUENCE FROM N.A.		RA Andrews N.C., Caput D., McKeon F.:	RT "p63, a p53 homolog at 3q27-29, encodes multiple products with		_	RN [2]		RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.			RC TISSUE=Skeletal muscle;	_	_			-	_				RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,	
5: sp_invertebrate:*						13: sp_vertebrate:*		17: sp_archeap:*		Fred. No. 15 The number of results predicted by chance to have a	and is derived by analysis of the total score distribution		SUMMARIES	of the state of th		e Match Length DB ID Description	100.0 487 4 Q9H3D2	98.0 470 II Q99JEI	98.0 487 11	96.3 483 11 088897	91.7 471 4 Q9NPH7 Q9np	91.7 516 4 Q9PlB7 Q9pl	91.7 555 4 Q9H3D3 Q9h3	91.7 641 4 075195	91.7 680 4 Q9H3D4	91.7 680 4 Q9UE10	91.0 538 11 Q99JD7	91.0 555 11	91.0 555 11 Q9QWZ0	91.0 663 11 Q99JE3	91.0	
									7	Pred.	and is				1,t	o. Score														14 2169	$\frac{15}{16}$ $\frac{2169}{2169}$,

Result Š ~

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61 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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                                                                                       Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-1363379; PubMed-11470269;
Bamberger C., Schmale H.;
"Identification and tissue distribution of novel KET/p63;
Variants.";
FEBS Lett. 501:121-126(2001).
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AJ277448; CAC37100.1;
HSSP; P04637: 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                               470 AA; 53399 MW; 96B7ED2FB30DD394 CRC64;
             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             099JE0 PRELIMINARY; PRT; 487 AA. 099JE0. 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                       98.0%; Score 2335; DB 11;
98.0%; Pred. No. 4.2e-198;
11ve 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P535UPPRESSR.
PRODOM; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
             01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.0
Matches 439; Conservative
                                                                            Rattus norvegicus (Rat)
                                                  TA1 KET gamma protein.
                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                    Nuclear protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
"Mutation and expression of the p51 gene in human lung cancer."; Neoplasia 1:71-79(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                              487;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 2383; DB 4; Length Best Local Similarity 100.0%; Pred. No. 2.5e-202; Matches 448; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   487 AA; 55687 MW; 86CC865BDF2643DD CRC64;
                    HOLDER LICENTIAL TOTALS)

-1 - SUBCLIGAR LOCATION NUCLEAR (BY SIMILARITY).

EMBL, AF12452B, AG45609.1; JOINED.

EMBL, AF12452B, AG45609.1; JOINED.

EMBL, AF12452B, AG45609.1; JOINED.

EMBL, AF12452B, AG45609.1; JOINED.

EMBL, AF12453B, AG45609.1; JOINED.

EMBL, AF1243B, AG45609.1; JOINED.

EMBL, AF1243B, AG45609.1; JOINED.
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EMBL, AF116755, AAF43486.1;
EMBL, AF116757, AAF43486.1; JOINED.
EMBL, AF116759, AAF43486.1; JOINED.
EMBL, AF116760, AAF43486.1; JOINED.
EMBL, AF116761, AAF43486.1; JOINED.
EMBL, AF116762, AAF43486.1; JOINED.
EMBL, AF116763, AAF43486.1; JOINED.
EMBL, AF116764; AAF43486.1; JOINED.
EMBL, AF116764; AAF43486.1; JOINED.
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PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 487 AA; 55687
                                                                                                                                                                    BAA32592.1
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Pfam; PF00870; P53; 1.
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AF116770; 7
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                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                              219
                                                                                                                                                                                                                                                                                                           DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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                                                                                                                                                                                                                                                                                 1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                          Gaps
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                                                                                                      Identification and tissue distribution of novel KET/p63 splice
                                                                                                                                                                                                                                       Length 487;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                      A688F392F32B3039 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
Last annotation update)
                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                      98.0%; Score 2335; DB 11;
98.0%; Pred. No. 4.4e-198;
iive 2; Mismatches 7;
                                                                                                                     FEBS Lett., 501:121-126(2001).
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILA-1- SIMILATY: BELONGS TO THE P53 FAMILY.
HSSP, 704637; 1YCS.
INTERPRO; 1PR02117; P53.
Pfam; PF00870; P53.
Pfam; PF00870; P53.
PRINTS: PR00386; P55SUPPRESSR.
PRODOM; PD002681; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                            STRAIN-Wistar; TISSUE-Tongue;
MEDLINE-21363378; PubMed-11470269;
                      Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                      487 AA; 55499 MW;
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08,
22,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.09
                                                                                              Bamberger C., Schmale H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08897;
01-NOV-1998 (TrEMBLrel. 00
01-NOV-1998 (TrEMBLrel. 00
01-OCT-2002 (TrEMBLrel. 27
TA*p63 gamma.
         TA2 KET gamma protein.
                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                             Nuclear protein.
SEQUENCE 487 A
                                                                                                               variants.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=98448055; PubMed=9774969;

A MEDLINE=98448055; PubMed=9774969;

Yang,A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.;

Tapis, a p53 homolog at 3q27-29, encodes multiple products with transactivating death-inducing, and dominant-negative activities.";

Mol. Cell 2:305-316(1998).

C -1 SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-1 SIMILARITY: BELONGS TO THE P53 FAMILY.

REMBL; AROT5434; AAC62639.1; -.

REMBL; AROT5434; AAC62639.1; -.

RESP; P04637; 1YCS.

REMBL; AROT5434; PO53.

REPROSE TO THE P53 FAMILY.

REMBL; PF00870; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLITVTLETRDGQVLGRRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 DSDLSDPWWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 12, Last annotation update)
P51 isoform Tap63delta (P51 delta protein).
HOMO sapiens (Human).
Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2296; DB 11;
Pred. No. 1.2e-194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00386; P53SUPPRESSR.
PRODOM; PD002681; P53; 1.
PROSTIE; P500348; P53; 1.
Nuclear protein.
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                                                                              NCBI_TaxID=10090;
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                SEQUENCE FROM N.A.
BEDILNE-20388515; PubMed-10935472;
Tani M., Shimizu K., Rawahara C., Kohno T., Ishimoto O., Ikawa S.,
Yokota J.;
                                                                                                                                                       "Mutation and expression of the p51 gene in human lung cancer.";
Neoplasia 1:77-79(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2185; DB 4; Length 471;
Pred. No. 8e-185;
3; Mismatches 7; Indels 1
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01-OCT-2000 (TrEMBLrel. 15, Created)
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94.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.1
Matches 416; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                      s.,
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                               O., Ikawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07553781103738B1 CRC64;
                                                                                                              SEQUENCE FROM N.A.
MEDLINE-20388515; PubMed-10935472;
MEDLINE-20388515; Rawahara C., Kohno T., Ishimoto Yokota J.;
    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%; Score 2185; DB 4; ilarity 94.1%; Pred. No. 9.1e-185; Conservative 3; Mismatches 7;
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    15, 1
22, 1
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AAF43488.1
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01-OCT-2000 (TrEMBLrel. 01-OCT-2002 (TrEMBLrel. P51 isoform TAp63beta.
                                                                                                                                                                                                                                                                                                                                                                                                                   PF00870; P53; 1
                                           Homo sapiens (Human).
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Best Local Similarity
Matches 416; Conserv
                                                                                                                                                                                                                                                                                                                                  AF116767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein
SEQUENCE 516
                                                                                                                                                                                                                                                                                                                                                                                          P04637;
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                                                                                          TISSUE-skeletal muscle;
MEDLINE-9832475; PubMed-9662378;
MEDLINE-98324755; PubMed-9662378;
Osada M., Obba M., Kawahara C., Ishloka C., Kanamaru R., Katoh I.,
Ikawa Y., Nimura Y., Nakagawara A., Obinata M.;
"Cloning and functional analysis of human p51, which structurally and functionally resembles p53.";
Nat. Med. 4:839-844(1998).
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Mutation and expression of the p51 gene in human lung cancer.";

"Mutation and expression of the p51 gene in human lung cancer.";

"I Neoplasia 1:1-79(1999).

-!- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE P53 FAMILY.

REMEL; AR016073; BAA32593.1;

REMEL; AR116756; AAR43487.1;

REMEL; AR116759; AAR43487.1;

REMEL; AR116759; AAR43487.1;

REMEL; AR116761; AAR43487.1;

MREMEL; AR116762; AAR43487.1;

MREMEL; AR116763; AAR43487.1;

MREMEL; AR116764; AAR43487.1;

MREMEL; AR116764; AAR43487.1;

MREMEL; AR116764; AAR43487.1;

MREMEL; AR116764; AAR43487.1;

MREMEL; AR116765; AAR43487.1;

MREMEL; AR11676
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MEDLINCE EROM N.A.
MEDLINCE-20388515; PubMed-10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
Yokota J.;
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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Pred. No. 1.2e-184;
3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           075195;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 09, Last seque
01-OCT-2002 (TrEMBLrel. 22, Last annof
P51 isoform TAP63ALPHA (P51B protein).
                                                                                                                                                                                                                                                                      : | | | : | | | 450 -----QTSIQSPSSYGNSSPP 465
                                                                                                                                                                                                                               421 LVEPRRETPKQSDVFFRHSKPP 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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EMBL; AF116767; AAF43487.1;
EMBL; AF116768; AAF43487.1;
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InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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PROSITE; PS00348; P53; 1.
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Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
I., Fig. a p53 homolog at 3427-29, encodes multiple products with
Lransactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
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Washaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555 AA; 62433 MW; E22874BE7DBABCBE CRC64;
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Last annotation update)
                                                                                              555 AA
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                                                                                                                                                                Created)
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Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOM; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
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                                                                                              PRELIMINARY;
                                                                                                                                                      01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
TA p63 beta.
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SEQUENCE 555 #
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Nuclear protein.
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                                                                                                                    MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                     DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                         PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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MEDILINE-98448095; bubmed-9774969;
WEDILINE-98484095; bubmed-9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3427-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Lymph;
Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AF124539; AAG45607.1;
EMBL; AF124529; AAG45607.1;
EMBL; AF124531; AAG45607.1; JOINED.
EMBL; AF124532; AAG45607.1; JOINED.
EMBL; AF124533; AAG45607.1; JOINED.
EMBL; AF124533; AAG45607.1; JOINED.
EMBL; AF124533; AAG45607.1; JOINED.
EMBL; AF124535; AAG45607.1; JOINED.
EMBL; AF124535; AAG45607.1; JOINED.
EMBL; AF124535; AAG45607.1; JOINED.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
p63).
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AAG45607.1;
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MEDLINE-99018225; PubMed-9799841;
Augustin M., Bamberger C., Paul D., Schmale H.;
"Cloning and chromosomal mapping of the human p53-related KET gene to chromosome 3427 and its murine homolog Ket to mouse chromosome 16.";
Mamm. Genome 9:899-902(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                            Length 680;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                          Score 2185; DB 4;
Pred. No. 1.3e-184;
3; Mismatches 7;
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AF124538; AAG45607.1; JOINED.
AF075430; AAC62635.1; -.
BC039815; AAH39815.1; -.
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                                                                                                                                                                                                                                                                                               680 AA; 76785 MW;
                                                                                                                                                                              PRINTS: PR00386; P53SUPPRESSR.
ProDom: PD002681; P53: 1.
SMART; SM00454; SAM: 1.
PROSITE; PS00348; P53: 1.
                                                                                                                                                                                                                                                                                                                                          Query Match 91.7%;
Best Local Similarity 94.1%;
Matches 416; Conservative
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                    Genew, HGNC:15979; TP63.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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                                                                    HSSP; P04637; 1YCS.
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DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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                                                                                                                                                                                                                                                                                                                                                                 160 SPSPAIPSNYDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPP 219
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                                                                                                                                                                                                                                                                                                                                                                                                     1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                           Length 680;
                                                                                                                                                                                                                   7; Indels
                                                                                                                                                              680 AA; 76776 MW; 6548A6F2187D852E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                       Ouery Match 91.7%; Score 2185; DB 4;
Best Local Similarity 94.1%; Pred. No. 1.3e-184;
Matches 416; Conservative 3; Mismatches 7;
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILATIVE BELONGS TO THE P53 FAMILY.

EMBL; Y16961; CAA76562.1; -.

HSSP; P04637; 1YCS.

INTERFO; IPR002117; P53.

INTERPO; IPR00160; SAM.

PERNYTS: PR00360; P53; 1.

PRNYTS: PR00366; P55SUPPRESSR.

PROMO PD002681; P53; 1.

SMARY; SM00454; SAM; 1.
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STRAIN-WISTAL: TISSUE-Tongue;
MEDLINE-21363378; Pubmed-11470269;
Bamberger C., Schmale H.;
Identification and tissue distribution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 LVEPRRETPKQSDVFFRHSKPP 442
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(TrEMBLrel. 17, L
(TrEMBLrel. 22, L
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01-OCT-2002 (TrEMBLre)
TA1 KET beta protein.
                                                                                                                                                   Nuclear protein.
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01-JUN-2001
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                          Gaps
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Identification and tissue distribution of novel KET/p63 splice
                                                                                                                                                          16;
                                                                                                                                    Length
                                                                                                                                                          Indels
                                                                                                          538 AA; 60326 MW; 66D0CA19786BF21B CRC64;
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Last sequence update)
Last annotation update)
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   P53 FAMILY
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MEDLINE=21363378; PubMed=11470269;
                                                         PRINTS; PR00366; P53SUPPRESSR. ProDom; PD002681; P53; 1. PR0SITE; PS00348; P53; 1. Nuclear protein. SEQUENCE 538 AA; 60326 MW;
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01-JUN-2001.(TrEMBLrel. 17,
01-OCT-2002 (TrEMBLrel. 22,
TAZ KET beta protein.
-i- SIMILARITY: BELONGS TO 1
EMBL; AJ277452; CAC37104.1;
HSSP; PO4637; 1YCS.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
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                                                                                                                                              Similarity
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                                                                                                                                              Best Local Sim
Matches 412;
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                                                                                                                     1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.
Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL, AF075435; AAC62640.1;
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                  16;
                                                                               555;
                                                                                Length
                                                                                                   Indels
                                                           65D8854E2387C74C CRC64;
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Last annotation update)
                                                                             Score 2169; DB 11;
Pred. No. 2.6e-183;
5; Mismatches 9;
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-0CT-2002 (TrEMBLrel. 22, Last anno
TA*p63 beta.
TRP63.
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       Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE: P500348; P53; 1.
Nuclear protein.
SEQUENCE 555 AA; 62426 MW; 61
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93.2%;
 InterPro; IPR002117; P53.
                                                                                                  412; Conservative
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MGD; MGI:1330810; Trp63.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
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                                                                                       Local Similarity
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Best Local S
Matches 412
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                         16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                         Indels
                                                                   059E034046EB8987 CRC64;
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01-JUN-2001 (TrEMBLrel. 17; Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
TAI KET alpha protein.
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FAMILY.
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                                                                                                          91.0%; Score 2169; DB 11;
93.2%; Pred. No. 2.6e-183;
11ve 6; Mismatches 8;
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FEBS Lett. 501:121-126(2001).
FISS Lett. 501:121-126(2001).
FISS Lett. 501:121-126(2001).
FISS Lett. 501:121-126(2001).
FISS LONG TO THE P53 FAA.
FISS P04637; 14C5.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
FRON FORO P59: P53SIPPRESSR.
FroDom; P0002681; P53; 1.
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STRAIN-Wistar; TISSUE-Tongue;
MEDLINE-21363378; PubMed-11470269;
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                                                                   555 AA; 62454 MW;
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 555 AA; 62454
                                                                                                        Query Match 91.0°
Best Local Similarity 93.2°
Matches 412; Conservative
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                                                                                        DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Lingual epithelium;
MEDLINE-97460723; PubMed-9315105;
Schmale H., Bamberger C.;
An novel protein with strong homology to the tumor suppressor p53.";
Oncogene 15:1363-1367(1997).
                                                                      16;
                                                 Score 2169; DB 11; Length 663;
Pred. No. 3.4e-183;
5; Mismatches 9; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLERR (BY. SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL: Y10258; CAB88216.1; -.
                             C953BBAC389D5B70 CRC64;
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Last annotation update)
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                                                91.0%;
93.2%;
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TISSUE-Lingual epithelium;
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
                                                         al Similarity 93.2
412; Conservative
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InterPro; IPR001660; SAM.
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                    Nuclear protein.
SEQUENCE 663 A
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Best Local S
Matches 412
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                                                                                                                                                                Gaps
                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 680;
                                                                                                680 AA; 76760 MW; AC45DABB88F61400 CRC64;
                                                                                                                            Score 2169; DB 11;
Pred. No. 3.5e-183;
5; Mismatches 9;
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he: 38.046 secs
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PRINTS: PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SWART; SM00454; SAM; 1.
                                                                                                                               91.0%;
93.2%;
                                                SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                              Best_Local Similarity 93.2
Matches 412; Conservative
                                                                                 Nuclear protein.
SEQUENCE 680 A
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(OTGEU) NNAJB 39A9 SIHT

tumour regulat

cell regulat protein #2 u oncogene p63 p63 protein

Human Human

Human

p51 protein

Human p63 homologu Human p63 protein Human kET protein. Human lung cancer Human p63 homologu Human p63 homologu

Human oncogene p5B Human oncogene p51 Human lung cancer

Нишап

Human lung cancer Human p53 homologu Mouse cell regulat Human cell regulat

oncogene p51 oncogene p63

Human Human

Rat KET protein. Human p63 protein

Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM protein

Run on:

p63 protein concogene p51 concogene p63

Human Human Human

Нишап

Human Human

lung cancer p53 homologu oncogene p51 oncogene p51 oncogene p51 cell regulat

Human

oncogene

oncogene p51 oncogene p63

Human

p40 protein

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Human cell regulatory protein p63, isoform deltaNp63 alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell regulatory protein; p63; hu-deltaNp63 alpha; human; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
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AAY05954
AAB11363
ABG95135
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ABP61915
ABB74995
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ABG95139
AAY43135
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ABB74993
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AAY50997
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97US-0062076
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(HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McKeon F, Yang A;
Homo sapiens.
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15-OCT-1997;
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AAY05956;
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  Human cell regulat
Human oncogene p63
Human oncogene p51
Human p63 protein
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p53 homologu
lung tumor a
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2301.535 Million cell updates/sec
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| SIDS1/gcdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS1/gcdata/geneseq/geneseqp-embl/AA1981.DAT:*
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1 MLYLENNAQTQFSEPQYTNL......FNFDMDARRNKQQRIKEEGE 586
                                                                         August 7, 2003, 09:31:28 ; Search time 40.4138 Seconds
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/SIDS1/gcgdata/geneseq/geneseq-embl/AA1994.DAT:*
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                    1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAB11357
AAB11357
ABP61909
AAY1032
AAB11317
ABF61869
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WPI; 1999-277595/23. N-PSDB; AAX58575.

lung cancer-

Human

3104 3104 3100 3087 3087 3087 3080 3080

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Result Š

Thu Aug

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour withch demonstrate certain sequence identity to known tumour campination is conserved between p73 and p53, and from faron-exon organisation is conserved between p73 and p53, and from known exon and intron staces for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their interventing intron. The human p53 gene was localised to chromosomal position intron. The human p53 gene was localised to chromosomal position of gamma forms, while p63 members differing in the N-terminus are designated as deltaN and TA forms, where the deltaN form lacks the transactivation domain. The present sequence represents human gong a clitan and mouse tissue. It demonstrates remarkably divergent post into human and mouse tissue. It demonstrate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63.

Cachexia) and neuronal differentiation and related degenerative disorders. p63 may also be implicated in haematopolesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 molyapetides (see AAVS8512-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such transgenic animals. New isolated p63 cell regulatory protein for, e.g. treatment of Claim 23; Fig 12; 161pp; English.

586 AA; Sequence

ö Length 586; Indels 100.0%; Score 3104; DB 20; 100.0%; Pred. No. 9.8e-244; 0; Mismatches Matches 586; Conservative Local Similarity Query Match

9 1 MLYLENNAQYQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS g οy 셤

YVEDPITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV 181 181

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DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 421 421

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481 QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR 540

541 ò

ABG95140 standard; Protein; 586

ABG95140;

04-DEC-2002 (first entry)

Human oncogene p63 isoform deltaN p63 alpha.

protein 90; Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein f85P-90; rheumatoid arthritis; cancer; haematopoietic disorder; call lymphona; B cell lymphona; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomocytic leukaemia; CMCL; acute lymphoblastic leukaemia; ALL; APL; MLI; solid tumour; papillary thyroid carcinoma; Paving's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.

Homo sapiens.

WO200269900-A2.

12-SEP-2002

01-MAR-2002; 2002WO-US06518.

01-MAR-2001; 2001US-272751P.

(CONF-) CONFORMA THERAPEUTICS CORP.

Fritz LC, Burrows FJ;

ö

WPI; 2002-698710/75. N-PSDB; ABS73332 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90

Disclosure; Page 346-348; 389pp; English.

The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I). treating annecrous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein or cellular protein isoforms (II) dependent on heat shock involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding concepenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. protein isoform in a patient heterozygous for (II). The method is useful to treating a disease e.g. hemmatopoletic discrder such as T or B cell ymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid surfaming and any serial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.

Sequence

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                                                                                                                                                                                                                                                                                                                          LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR 300
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                                                                                           TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative disease; cellular protein isoform; heat shock protein 90; HBP-90; rheumatoid arthritis; cancer; heamatopoitetic disorder; T cell lymphona; B cell lymphona; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML; acute lympholastic leukaemia; ALL; APL; NLL; solid tumour; papillary thyroid carcinoma; Eving's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection
                                                         VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                   YVEDPITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV
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  Length 586;
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Pred. No. 9.8e-244;
Mismatches 0;
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Best Local S
Matches 586
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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein or cellular protein isoforms (II) dependent on heat shock protein furbly treating cells expressing (II) involving administering HSPO-101/Lto. The method is useful for creating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein or cellular protein isoform in a patient heteroxygous for (II). The method is useful protein isoform in a patient heteroxygous for (II). The method is useful isoform disease e.g. hemmatopoietic disorder such as Tor B cell ymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, I ymphoma, chronic myeloid leukaemia (CML), ALL, ALL, ALL, ALL, and CMML, I will and sease of the protein contained the sease of the method is useful the sease of the method (CML), ALL, ALL, ALL, ALL, and CML, and CML,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein
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                                                                                                                                                                                                   Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.9%; Score 3100; DB 23; 99.8%; Pred. No. 2.1e-243; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                          Disclosure; Page 331-333; 389pp; English.
                                                    CORP
                                                  (CONF-) CONFORMA THERAPEUTICS
01-MAR-2001; 2001US-272751P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.9
Best Local Similarity 99.8
Matches 585; Conservative
                                                                                                    Fritz LC, Burrows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     586 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQQUULLIA
                                                SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQ 360
                                                                                                                                                                                                                                  SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG 420
                                                                                                                                                                                                                                                                                                                                             Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer
                                                                                                                                                Kalos MD, Henderson RA;
cham M, Fanger GR, Vedvick TS;
                                                                                                                                  LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                   YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV
                                                                                                                                                                                                                                                                                               QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
                                                                                                                                                                                                                                                                                  DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                               GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
                                                                                                                                                                                                                                                                                                                                                                                            Human lung cancer associated protein sequence SEQ ID NO:338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Durham M, Fange
Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ang A, Skeiky YAW, Li SX,
', Fanger N, Retter MW, Dur
Watanabe Y, Peckham DW, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP61909 standard; Protein; 586
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07-MAY-2001; 2001US-0850716.
28-JUN-2001; 2001US-0897778.
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N-PSDB; ABQ92432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200247534-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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28-JUN-2001;
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McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-0CT-2002
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                        This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polyucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
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                                                                                                                                                                                                                                             Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic; vaccine; detection.
            Q1EHYSMDDLASLKIPEQFRHAIWKG1LDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
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                                                         Indels
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Pred. No. 2.4e-242;
1; Mismatches 2;
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                                                                                                                                              AAB11357 standard; Protein; 586
                                                                                                                                                                                                                      Human p63 protein isoform #1.
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99US-0466396.
99US-0476496.
2000US-0480884.
2000US-0510376.
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11 Similarity 99.5%;
583; Conservative
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                                                                                                                                                                                              (first entry)
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17-DEC-1999;
30-DEC-1999;
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22-FEB-2000;
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Best Local
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                                                              The present invention describes isolated human lung carcinoma polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by cobtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide and coligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABB02145 represent sequences used in the exemplification of the present invention.
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Example 2; Page 326-328; 381pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes human lung tumour proteins. Human lung activaties, and polynucleotides have cytostatic and immunostimulant activaties, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating ing cancer or stimulating an immune response. ABL88959 to ABL8930 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                       tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLYLENNAQTQFSEPQYINLGLLNSMDQQIRNGSSSTSPYNTDHAQNSVTAPSPYAQPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVEDPITGROSYLVPYEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for treating
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NO:338
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  n
protein SEQ
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er N, Retter MW, Marnerakis M,
er D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor polypeptides,
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Pred. No. 2.4e-242;
; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune response
p53 homologue isoform, p63 (L530S)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer or stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotides encoding lung
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2000US-0643597.
2000US-0662786.
2000US-0685696.
2000US-0735705.
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99.5%;
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Best Local Similarity 99.5
Matches 583; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fanger N,
Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-090513/12.
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                                                           immune response
                                                                                                                                            WO200200174-A2.
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12-DEC-2000;
07-MAY-2001;
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                                                   61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment; human; tumor; immunogenic; cytostatic;
                                                                 SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                       DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                                                                                                                                                                                                                                                                                                                                    QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
 1 MLYLENNAQTQFSEPQYTNIGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                          YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV
                                                                                                                                                                                                                                                               SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQQHQHLLQKQTSIQ
                                                                                                                                                                                                                                                                                                                 SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTT1PDGMGAN1PMMGTHMPMAG
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99US-0466396.
99US-0476496.
2000US-0480884.
2000US-0510376.
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17-DEC-1999;
30-DEC-1999;
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                                                                                                                                                         The invention provides isolated human lung tumor nucleic acids and polypeptides. The polypeptides can be used for the treatment of lung cancer. The polypeptides and polynucleotides can be used to stimulate T cells or antigen presenting cells for use in the treatment of lung cancer. The polypeptides and monoclonal antibodies specific for the polypeptides and monoclonal inthe the development of lung cancer. Agents which bind the polypeptides can be used for detecting lung cancer and for monitoring the progression of lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated lung tumor polynucleotides, used to develop products for
the treatment, prevention and monitoring the progression of lung cancer
DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                                                             QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
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                                                                                                                                                                                               GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                                                                                                                             tumor; lung cancer; T cell stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 3080; DB 20;
Pred. No. 8.8e-242;
2; Mismatches 2;
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                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                      AAY41032 standard; protein; 586
                                                                                                                                                                                                                                                                                                                                                                 Human lung tumor antigen L503S
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99.38;
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98US-0123912.
98US-0123933.
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                                                                                                                                                                                                                                                                                                                                        (first entry)
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es 582; Conserv
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Homo sapiens WO9947674-A2

lung

Human;

07-DEC-1999

AAY41032;

AAY41032 RESULT

17-MAR-1999;

23-SEP-1999

18-MAR-1998; 27-JUL-1998;

27-JUL-1998;

8-MAR-1998;

286

Sequence

Query Match

Best Loca Matches

SG, Wang

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TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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                                                                                                          This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting calls expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QIEHYSMDDLASLKIPEQFRHAIWKG1LDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
                           Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung
                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                    Length 586;
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Pred. No. 8.8e-242;
2; Mismatches 2;
                                                                                 Claim 3; Page 163-164; 261pp; English
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es 582; Conservative
                                                                                                                                                                                                                                                             development of cancer.
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The present invention describes isolated human lung carcinoma polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in presence of a cancer in the patient. (I) and (II) are useful in a pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                       Fanger GR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                 Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                         Henderson
                                 Human lung cancer associated protein sequence SEQ ID NO:152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                      / YAW, Li SX, Kalos MD, He
Retter MW, Durham M, Fange
Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3080; DB 23;
Pred. No. 8.8e-242;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 253-254; 381pp;
                                                                                                                                                                                                                                                                                                                                        Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.2%;
ilarity 99.3%;
Conservative
                                                                                                                                                                                                                                 12-DEC-2000; 2000US-0735705.
07-MAY-2001; 2001US-0850716.
28-JUN-2001; 2001US-0897778.
                                                                                                                                                                                                  30-NOV-2001; 2001WO-US47576
07-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                               Wang T, Wang A, Koneill PD, Fanger N, Watanabe Y,
                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-583465/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     586 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABQ92292
                                                                                                                                  WO200247534-A2.
                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or
                                                                                                                              Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                      SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQ
                                                            SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                               DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                       Polynucleotides encoding lung, tumor polypeptides, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fanger GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henderson
                                                                                                                                                                        GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                                                                                                                                                                                              Human lung tumour L530S protein sequence SEQ ID NO:152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky YAW, Li SX, Kalos MD,
er N, Retter MW, Marnerakis M,
er D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung cancer or stimulating an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 246-247; 374pp; English.
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                                                                                                                                                                                                                           ABB74949 standard; Protein; 586
                                                                                                                                                                                                                                                                                                                                                                                                           20000S-0643597.
20000S-0662786.
20000S-0685696.
20000S-0735705.
20010S-0850716.
                                                                                                                                                                                                                                                                                                                                                                                           2000US-0606421.
2000US-0630940.
                                                                                                                                                                                                                                                                                                                                                                          28-JUN-2001; 2001WO-US21065.
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fanger N,
Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-090513/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-090513/
N-PSDB; ABL49106.
                                                                                                                                                                                                                                                                                                       response
                                                                                                                                                                                                                                                                                                                                        WO200200174-A2
                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-2000;
02-AUG-2000;
21-AUG-2000;
15-SEP-2000;
09-OCT-2000;
                                                                                                                                                                                                                                                                                                                         Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang T, Wang
McNeill PD,
Vedvick TS,
                                                                                                                                                                                                                                                             01-MAY-2002
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07-MAY-2001;
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ABB74949
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                                                                                                                                                                                                                     TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                          SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
                                                                                                                                                         1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                       VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                                                                                                                          LGRRCFEARICACPGRDRKADEDSIRKOOVSDSTKNGDGTKRPFRONTHGIOMTSIKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                          0;
                                                                                            Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse cell regulatory protein p63, isoform deltaNp63 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell regulatory protein; p63; mu-deltaNp63 alpha; mouse; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                       Score 3080; DB 23;
Pred. No. 8.8e-242;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY05962 standard; Protein; 586 AA
                                                                                            99.2%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US21992
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                                                                                                         al Similarity 99.3
582; Conservative
                                                             586 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09919357-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-1999
                              invention.
                                                                                         Query Match
Best Local S
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                                                               Sequence
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                                                                                                         Best Loc
Matches
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The present sequence represents a human p51 protein, which is related to p53 and has cell proliferation regulation and tumour suppression activity. The p51 gene can be used in the investigation, diagnosis and treatment of diseases such as concer, with which the p53 family cell proliferation regulation is associated. The p51 protein may be used for screening potential agonists and antagonists of its regulatory function,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigation and proliferation
                     $QSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAG
                                                                                               QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
                                                                             DMNGLSPTQALPPPLSMPSTSHCTPPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell proliferation; regulation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20; Length 641;
                                                                                                                                                                                                                                                    GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New p53 related human gene p51, useful for diagnosis, treatment of cancers and screening for potential cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142..321
/label- DNA_binding_domain
353..397
/label- oligomerisation_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label = transactivation_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.7%; Score 3033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 152-154; 163pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    AAY45247 standard; Protein; 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Obinata M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; p51; p53 related gene;
tumour suppression; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-JP01512.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human p51 protein B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       641 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAKA ) OTSUKA PI
(IKAW/) IKAWA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ25771
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                                                                                                                                                                                                                                                                                                                                                                                                      AAY45247;
                                                                                                                                                                                                                                541
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                                                                                                                                                                                                                                                                      The present invention concerns the discovery of a new family of cell regulatory proteins (CRPB) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using cC amplified CDNA possessed a truncated N-terminus, i.e. the transactivation domain was absent. Additional splice variants were identified by screening a cDNA library with a probe corresponding to exons 5-9 of p63. At least 6 different isotypes exist. Splice to and gamma forms, while p63 embers differing in the N-terminus are corresponding at the C-terminus are designated as deltan and TA forms, where the deltan form lacks the castignated as deltan and TA forms, where the deltan form lacks the corresponding. The present sequence represents mouse p63 isotype mu-deltany63 alpha. p63 was detected in a variety of cisotype mu-deltany63 alpha. p63 was detected in a variety of activities, such as the ability to transactivate p53 reporter genes condinduce apoptosis. Cessation or down-regulation of p63 expression differentiation, both benign and necoplastic. Deltan isotopes of p63 cact as dominant negatives towards transactivation by p53 and p63. CC act as dominant negatives towards transactivation by p53 and p63. CC act as dominant negatives towards transactivation by p53 and p63. CC cachexia) and neuronal differentiation and related degenerative cachexia) and neuronal differentiation and related degenerative condexia) and neuronal differentiation and in the production of processes, in detection and diagnosis, and in the production of transgentc animals.
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Pred. No. 1.2e-240;
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98.5%;
98US-0087216
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Matches 577; Conservative
                                                         (HARD ) HARVARD COLLEGE.
                                                                                                                                 WPI; 1999-277595/23
                                                                                             Yang A;
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                                                                                                                                                     N-PSDB; AAX58581
 29-MAY-1998;
                 15-OCT-1997;
                                                                                             McKeon F,
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Best Local Similarity 100.
Matches 572; Conservative
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                 N-PSDB; AAX58572
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                                                                               PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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                Gaps
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                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cell regulatory protein p63, isoform huTAp63 alpha
        Pred. No. 6.6e-238;
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97US-0062076.
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       Best Local Similarity 100.
Matches 572; Conservative
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15-OCT-1997;
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97.7%; Score 3033; DB 20; 100.0%; Pred. No. 6.6e-238; ive 0; Mismatches 0;

Length 641;

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victor wence certain sequence identity to known tunnour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron islaes for these 2 genes, it was possible to chromosomal position of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position of affering at the C-terminus have been designated as alpha, beta and differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are cessionated as delitan and A forms, where the deltan form lacks the transactivation domain. The present sequence represents human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 and p63.

Cc act as dominant negatives towards transactivation by p53 and p63.

Cc act as dominant negatives towards transactivation by p53 and p63.

Cc achexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see AAX05972-83) and anti-p63 antibodies of the invention can be used to consider the production of processes, in detection and diagnosis, and in the production of transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour
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                                                                                                                                                            e.g. treatment
                                                                                                                                                 New isolated p63 cell regulatory protein for,
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WPI; 1999-277595/23.
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GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 314
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                                  LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein gisp-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphona; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphonastic leukaemia; ALL; APL; NBL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                              PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
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LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
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                                                                                                                                                                                                                                                                                                                                 Human; cytostatic; gene therapy; p53; human tumour.
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/label- DNA_binding_domain
353..397
/label- Oligomerisation_domain
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/label- Transactivation_domain
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                                                                                                           610 TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 641
                                                                                           555 TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
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N-PSDB; AAF86589.
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proteins (1), treating cancerous cells containing (1) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (11) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (11) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (c.g. Theumatof at their social associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterosyous for (II). The method is useful (for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, CC or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, inposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous Disclosure; Page 352-354; 389pp; English.

641 AA; Sequence

Gaps ; Length 641; Indels 97.7%; Score 3033; DB 23; 100.0%; Pred. No. 6.6e-238; ive 0; Mismatches 0; Best Local Similarity 100.0 Matches 572; Conservative Query Match ŏ

74 15 POYTNIGILNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN

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PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP 250 195

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255 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR

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LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK 494 435

495 IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ

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554

TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586

Search completed: August 7, 2003, 09:46:26

Job time : 42,4138 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54; Search time 16.1655 Seconds

(without alignments)
1533.769 Million cell updates/sec
Perfect score: US-09-538-106-16
Sequence: 1 MLYLENNAQTQFSEPQYTNL......FNFDMDARRNKQQRIKEEGE 586
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 328717 seqs, 42310858 residues
Total number of hits satisfying chosen parameters: 328717
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
7: /cgn2_6/ptodata/1/iaa/pcxfiles1.pep:*
7: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RIES		3-59	2 - 61	6-42	3-59	0-88	2 - 61	6-42	3-59	2 - 61	6-42	3-59	2-61	6-42	3-59	2 - 61	6-42	3-59	2-61	6-42	7-19	3-29	7-19	542-615A	6-42	3-59	2 - 61	606-42
SUMMARIES		9-643	9-542	09-606-421B	9-64	9-48	9-545	09-6	9-64	9-54	09-60	-09-643	9-54	09-6	9-64	9-54	09-6	-09-643	9-54	-09-606-421B	9-277	9-64	-09-277-196			9	9-54	
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ALIGNMENTS

Db 301 SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQHQHLLQKQTSIQ 360	Qy 361 SPSSYGNSSPPLNKANSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPWMGTHMPWAG 420	Qy 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480	Oy 481 OIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR 540	Qy 541 GERVIDAVRFTLRQTISFPRDEWNDFNFDWDARRNKQQRIKEEGE 586 	RESULF 3 US-09-606-421B-338	PRESENT INFORMATION REPLICANT: Ren, 1140 R
DD 241 LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIOMTSIKKRR 300	QY 301 SPDDELLYLPVRGRETYEMLLKIKESLELMOYLPQHTIETYRQQQQQQHQHLLQKQTSIQ 360 	Qy 361 SPSSYGNSSPPLNKMNSMNKLPSVSOLINPOORNALTPTTIPDGMGANIPMWGTHMPMAG 420 	QY 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480	QY 481 QIEHYSMDDIASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR 540	Qy 541 GERVIDAVRFTLRQFISFPERDEWNDFNFDWDARRNKQQRIKEEGE 586 	RESULT 2 Sequence 318, Application US/09542615A APPLICANT: Wang, Michael D. APPLICANT: Wang, Michael D. APPLICANT: Hosken, Mancy A. APPLICANT: Hosken, Mancy A. APPLICANT: Hosken, Mancy A. APPLICANT: September 2.01011.455G8 CURRENT TILK DATE: 2000-04-14 APPLICANT: Passence: 2000-04-14 APPLICANT: Basence: 2000-04-14 APPLICANT: Passence: 2000-0

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Db 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480 Qy 481 QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR 540	RESULT 7 US-09-606-421B-152 Sequence 152, Application US/09606421B Sequence 152, Application US/09606421B Sequence 152, Application US/09606421B GENERAL INFORMATION: APPLICANT: Wang, Tongtong APPLICANT: Ralos, Michael D. APPLICANT: Hosken, Nancy APPLICANT: Hosken, Nancy APPLICANT: Hosken, Nancy APPLICANT: Stager, Gary R. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE SECOND A.S. TITLE REFERENCE: 210121.45509 CURRENT FILING DATE: 2000-66-28 SOFTWARE PERSON FOR MINDOWS VERSION 3.0 SEQ ID NO 152 LENGTH: 586 TYPE: PRT TYPE: PRT CORRANTSM: Homo sapien US-09-666-421B-152	Query Match 99.2%; Score 3080; DB 4; Length 586; Best Local Similarity 99.3%; Pred. No. 1.38-277; Indels 0; Gaps 0; Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0; DD 1 MLYLENNAQTOFSEPOTYNLGILNSMOQIONGSSSTSPYNTDHQNNSYTAPSPYAQPSS 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
361 SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG 420 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTGCLTTY 480 [111111111111111111111111111111111111	GENVIDAVRFILROITSFFPRDEWNDFNFDWDARRNKOORIKEEGE A-152 2, Application US/09542615A 5518256 DRWATION: Wang, Tongtong Fan, Ligun Ralos, Michael D. Bangur, Chaitanya S. Hosken, Nancy A. Fanger, Gary R. Fanger, Gary R. WYENTION: WYENTION: WYENTION: WYENTION: SECTION WINGHER: US/09/542,615A LING DATE: 2000-04-14 SECTION NOWBER: US/09/542,615A LING DATE: 2000-04-14 SECTION NOWBER: SECTIO	99.2%; Score 3080; DB 4; Length 586;

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APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FITEL OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
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CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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Wang, iqun
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Skeiky, Yasi
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Pred. No. 8e-273;
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APPLICANT: FADGET, GATY R.

TITLE OF INVENTION: COMPOUNDS AND METHODS .

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG C.

FILE REFERENCE: 210121.45508

CURRENT APPLICATION NUMBER: US/09/542,615A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS 350

SOFTWARE: FASTSEQ for Windows .

SEQ ID NO 339

LENGTH: 641

TYPE: PRT
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US-09-542-615A-339
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GENERAL INFORMATION:
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Pred. No. 8e-273;
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APPLICANT: Kano, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aijun
CONTRESTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: NUMBER: US/09/606,421B
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
TONNATCH HOMO SENTENS
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US-09-606-421B-339
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Pred. No. 8e-273;
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TITLE OF INVENTION: COMPOSITIONS AND METHOD:
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG C
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
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McNeill, Patricia D.
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Fanger, Gary R.
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CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FESTSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
FILE REFERENCE: 210121.455C8
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APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
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APPLICANT: ASCIPTIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF EGO ID NOS: 358
NUMBER OF EGO ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
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GENERAL INFORMATION:
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya
APPLICANT: Hosken, Nancy
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99.8%;
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Pred. No. 2.1e-27
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Mismatches
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314 348 254 288

494

528 434 468 374 408

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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Mancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Menderson, Robert A.
APPLICANT: Meneill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHOD
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG C
FILLE REPERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3443
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US-09-643-597-343
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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TYPE: PRT
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                                                                                                                                                                                                                                      181 YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                                                             121 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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10. 6426072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
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                                                                                                           SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                    SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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Pred. No. 1.6e-216;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE THERAPY
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METITLE OF INVENTION: AND DIAGNOSIS OF FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTMARE: FastSEQ for Windows Versic SEQ ID NO 343
FENCTH: 461
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-343
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Best Local
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                                                                                                               SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
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DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                                       SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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Pred. No. 1.6e-216
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Search co completed: August ne : 18.1655 secs 7, 2003, 09:54:54

> 420 420

240

RESULT 15
US-09-542-615A-343
; Sequence 343, Application
; Patent No. 6518256
; GENERAL INFORMATION:

US/09542615A

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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length: 2000000000
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3104
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                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                   /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
Д	3087	99.5	586	9	US-09-735-705-338	Sequence 338, App
2	3087	99.5	586	10	US-09-850-716A-338	338
ω	3087	99.5	586	10	US-09-897-778-338	•
	3080	99.2	586	9	US-09-735-705-152	Sequence 152, App
5	3080	99.2	586	10	US-09-850-716A-152	Sequence 152, App
6	3080	99.2	586	10	US-09-897-778-152	Sequence 152, App
7	3080	99.2	586	11	US-09-466-396A-152	Sequence 152, App
8	3029	97.6	641	9	US-09-735-705-339	Sequence 339, App
9	3029	97.6	641	10	US-09-850-716A-339	Sequence 339, App
10	3029	97.6	641	10	US-09-897-778-339	Sequence 339, App
11	3025	97.5	680	9	US-09-735-705-342	Sequence 342, App
12	3025	97.5	680	10	US-09-850-716A-342	Sequence 342, App
13	3025	97.5	680	10	US-09-897-778-342	Sequence 342, App
14	2421	78.0	461	9	US-09-735-705-343	Sequence 343, App
15	2421	78.0	461	10	US-09-850-716A-343	
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679.5	692	694	698	700.5	701	703.5	707.5	707.5	707.5	707.5	707.5	707.5	707.5	707.5	1279.5	1741	1741.5	1813	1813	1813	1872	1872	1872	1872	1893	2350	2350	2350	
21.9		•									•	22.8	•	•	٠	•	56.1	58.4	58.4	58.4		60.3			61.0			75.7	
374	381	394	390	353	390	401	428	393	393	393	393	393	393	393	420	636	635	448	448	448	356	356	356	356	426	516	516	516	
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US-09-968-851-28	US-09-968-851-36	US-10-155-059-4	US-10-160-290-3	US-10-146-473-78	US-10-038-010-6	-851-	US-10-076-691-2	US-10-160-290-2	٠	US-09-860-286-9	US-09-029-327-4	US-09-860-211-9	US-09-732-384-3	US-09-776-695-32	US-10-274-874-20	US-09-732-384-10	US-10-155-059-3	US-09-897-778-340	US-09-850-716A-340	US-09-735-705-340	US-10-274-874-2 .	US-09-897-778-341	US-09-850-716A-341	US-09-735-705-341	US-10-274-874-19	US-09-897-778-344	US-09-850-716A-344	US-09-735-705-344	
28,			Sequence 3, Appli	Sequence 78, Appl	Sequence 6, Appli		Sequence 2, Appli	2	Sequence 4, Appli	Sequence 9, Appli	4	Sequence 9, Appli	e u	32,	Sequence 20, Appl	10	ω	340,	e 34	40	Sequence 2, Appli	Sequence 341, App	341,	Sequence 341, App	Sequence 19, Appl	.~	•		J.J

ALIGNMENTS

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; SOFTWARE: FastSEQ for Wi
SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-338
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US-09-735-705-338; Ap
                                                             Query Match
Best Local Similarity
Matches 583; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 338, Application US/09735705 Patent No. US20020052329A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                     APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                 1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
MLYLENNAQTQFSEPQYTNLGLLNSMDQQIRNGSSSTSPYNTDHAQNSVTAPSPYAQPSP 60
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Fanger, Gary R.
Li, Samuel X.
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Tan, Liqun
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                                                                Conservative
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                                                             Score 3087; DB 9;
Pred. No. 7.9e-248;
1; Mismatches 2;
                                                                                            Length 586;
                                                                Indels
                                                               0;
                                                             Gaps
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APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patticia D.
APPLICANT: McNeill, Patticia D.
APPLICANT: Metter, Marc W.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716A-338
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US-09-850-716A-338
; Sequence 338, Application |
; Patent No. US20020115139A1
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Similarity 99.5%;
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                                                                                                                                                                Score 3087; DB 10;
Pred. No. 7.9e-248;
""smatches 2;
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455016
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
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APPLICANT: Marnerakis, Man
APPLICANT: Marnerakis, Mar
APPLICANT: Fanger, Gary R
APPLICANT: Vedvick, Thomas
APPLICANT: Carter, Darricl
APPLICANT: Watanabe, Yosh
APPLICANT: Henderson, Rob
APPLICANT: Peckham, David
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Best Local
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7.9e-248;
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SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-735-705-152
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APPLICANT: Wang, To
APPLICANT: Fan, Liq
APPLICANT: Kalos, M
APPLICANT: Bangur,
APPLICANT: Hosken,
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
CONTRABER: FRESTER OF THE METHOD SEQ ID NOSE AND SECOND SE
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                                                                         TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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Fanger, Gary R.
Li, Samuel X.
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 McNeill, Patricia D.
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Pred. No. 3e-2.
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GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
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Application US/09850716A
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GENERAL INFORMATION:

APPLICANT: Kalos, Michael D.

APPLICANT: MCNeill, Patricia D.

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C15

CURRENT APPLICATION NUMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF 5EQ ID NOS: 440

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 152

LENGTH: 586

TYPE: PRT

ORGANISM: Homo sapien

VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPSSHLIRVEGNSHAQ Score 3080; DB 1 Pred. No. 3e-247; 2; Mismatches 2; Indels 0; Gaps 240 180 120 300 180 60

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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
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Best Local
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APPLICANT: Warner
APPLICANT: Fange
APPLICANT: Vedvic
APPLICANT: Carte
APPLICANT: Watan
APPLICANT: Waten
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                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
                                                                                                                                                                                                                                                           Local
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Similarity 99.3%;
                                                   YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                       TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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                                       YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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Watanabe, Yoshihiro
Henderson, Robert A.
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Vedvick, Thomas S.
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Pred. No. 3e-247;
2; Mismatches
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PUBLICATION NO. US20030119763A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FO
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C4
CURRENT FILING DATE: 199-12-17
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
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                                                   LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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                                                                                                      LGRRCFEARTCACPGRDRKADEDSTRKQQVSDSTKNGDGTKRPFRQNTHGTQMTSIKKRR
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Pred. No. 3e-247;
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420 420 360 360 300 300 240 240 180 180 120 60

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Sequence 33 Application US/09735705 Patent No. US20020052399A1 Patent No. US2002005239A1 PATENT NO. US2002005239A	Qy 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
US-99-850-716A-339 IS-99-850-716A-339 IS-99-850-716A-330 IS-99-850-716A-339 IS-99-850-716A-330 IS-99-850-716A-300 IS-99-	Db 430 MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 489 Qy 435 LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTGGLTTIYQIEHYSMDDLASLK 494

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US-09-897-778-339
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Best Local S
Matches 571
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LENGTH: 641
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APPLICANT: Fange.
APPLICANT: Fange.
APPLICANT: Vedvi.
APPLICANT: Carte.
APPLICANT: Watan
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APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Panger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
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-09-897-778-339
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                       GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPYRGR
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                                                                                                      MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
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IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
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Henderson, Robert A.
Peckham, David W.
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Pred. No. 5.9e-243;
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: AND DIAGNOSIS OF
FILE REFERENCE: 210121.455014
CURRENT APPLICATION NUMBER: US/09/735
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Versic
SEQ ID NO 342
LENGTH: 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: Homo sapiens US-09-735-705-342
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US-09-735-705-342
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Best Local Sim
Matches 571;
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APPLICANT:
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              LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK 494
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                                                                            MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
                                                                                                                                         ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK
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Wan, Liqun
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                                                             MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
                                                                                                                       ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK
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Fanger, Gary R.
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GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 680
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US-09-850-716A-342
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US-09-850-716A-342
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                 TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
                                                                IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
                                                                                                                           LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
                                                                                                                                                                        MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
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                                                IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
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Pred. No. 1.4e-242;
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US-09-897-778-342
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CURRENT FILING DATE: 2001-06-28 .
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 342
LENGTH: 680
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APPLICANT: Warner
APPLICANT: Fanger
APPLICANT: Vedvic
APPLICANT: Carter
APPLICANT: Watana
APPLICANT: Hender
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Matches 571;
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                TISEPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
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Vedvick, Thomas S.
Carter, Darrick
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408 374 468 348

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHC
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TITLE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Wind
SEQ ID NO 343
LENGTH: 47
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-343
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             DMNGLSPTQALPPPLSMPSTSHCTPPPPPYPTDCSIV 456
                                                                     SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                               SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLLQKQTSIQ
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DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
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Fan, Liqun
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; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 343
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APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIACHOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
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                                                                                                          LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                       SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                SPSSYGNSSPPLNKMNSMNKLPSYSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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pred. No. 1.1e-192;
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RESULT 15 US-09-850-716A-343

Sequence 34 Patent No.

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Application US/09850716A

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Result
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A; Molecule type: mRNA A; Residues: 1-396 < DEF>

JH0631 cellular tumor antigen p53 - rainbow trout C;Species: Oncorhynchus mykiss (rainbow trout) C;Date: 10-Sep-1999 #sequence_revision 10-Sep- C;Accession: JH0631 R;de Fromentel, C.C.; Pakdel, F; Chapus, A.; Gene 112, 241-245, 1992 A;Title: Rainbow trout p53: cDNA cloning and b A;Reference number: JH0631; MUID:92210006; PMI A;Accession: JH0631 A;Molecule type: mRNA A;Molecule type: mRNA	RESULT 1	45 122.5	44 · 122.5	42 123		40 123	12		<u></u>	36 124			33 124.5			30 124.5
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JH0631 Cellular tumor antigen p53 - rainbow trout C;Species: Oncorhynchus mykiss (rainbow trout) C;Secession: JH0631 R;de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T Gene 112, 241-245, 1992 A;Title: Rainbow trout p53: CDNA cloning and biochemical characterization. A;Reference number: JH0631; MUID:92210006; PMID:1339362 A;Accession: JH0631 A;Molecule type: mRNA	ALIGNMENTS	B86292	T23472	T34454 T42730	T18235	T15446	A45183	A48184	B53689	I38972	A44068	\$45251	T04518	H85335	JC7619	JS0304
t_change 10-Sep-1999 ; May, P.; Soussi, T. l characterization.		F7H2.12 protein -	hypothetical prote	Bassoon protein -	transcription acti	hypothetical prote	TBP-associated fac	transcription init	homeotic protein C	hypoxia-inducible	cell pattern forma	SNF2alpha protein	hypothetical prote	hypothetical prote	hypoxía-inducible	developmental cont

QY 339 ETYRQQ 344 : : Db 360 DKYRQK 365	QY 284 FRQ-NTHGIOMTSIKKRRSPDDEL ::	Qy 227 ILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQO- : :	QY 167 PSHLIRVEGNSHAQYVEDPITGRQSVLV	QY 107 LYCQIAKTCPIQIKVMTPPPOGAVIRAN : : : : 121 LFCQLAKTCPVQIVVDHPPPPGAVVRAL	Qy 49 VTAPSPYAQPS-STEDALS-PSPAIPSN	Query Match 27.0%; Score 839.5; Best Local Similarity 55.2%; Pred. No. 8e-5 Matches 169; Conservative 47; Mismatches	A;Cross-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829 A;Experimental source: liver C;Comment: This protein is the product of a tumor suppressor gene, p53, C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; F;164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
	FRQ-NTHGIOMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 338 :: : : : : : : : : : : : :	ILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRP 283 : : : :	PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRP 226 : :: :	LYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREENEGQIAP 166 - - - - -	VTAPSPYAOPS-STFDALS-PSPAIPSNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKK 106 : : :	27.0%; Score 839.5; DB 1; Length 396; 55.2%; Pred. No. 8e-51; ative 47; Mismatches 79; Indels 11; Gaps 6;	A;Cross-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829 A;Experimental source: liver C;Comment: This protein is the product of a tumor suppressor gene, p53, whose inactiv C;Comment: This protein is the product of a tumor suppressor gene, p53, whose inactiv C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho F;164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

RESULT 2 A29376

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A;Title: Nucleotide sequence of a cDNA encoding the chicken A;Reference number: S02193; MUID:89083584; PMID:3060861 A;Accession: S02193 A;Molecule type: mRNA A;Residues: 1-367 <SOU>
                                                                                                                                                                        cellular tumor antigen p53 - chicken
N;Alternate names: nuclear oncoprotein p53
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S02193
R;Soussi T; Begue, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
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A;Residues: 1.293,295-363 <HOE>
A;Residues: 1.293,295-363 <HOE>
A;Cross references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
A;Cross reference, J; Wedlich, D; Montenarh, M.; Knochel, W.
Submitted to the EMBL Data Library, March 1994
A;Reference number: S72313
A;Accession: S72313
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A;Title: Cloning and characterization of a cDNA from Xernitle: Cloning and Cha
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S02193
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C;Superfamily: cellular tumor antigen p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nu: C;Keywords: 13,217/Binding site: zinc (Cys, His, Cys, Cys) *status predicted F;150,153,213,217/Binding site: phosphoryl-RNA (Ser) (covalent) *status predicted F;362/Binding site: phosphoryl-RNA (Ser) (covalent) *status predicted
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A; Accession: A29376
A; Molecule type: mRNA
A; Molecule: 1-563 < SOU>
A; Residues: 1-563 < SOU>
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A; Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HOW>
A; Cross-references: EMBL: X77546; NID: 9468513; P
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A; Title: Overexpression of wild-type
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R;Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
   type: mRNA: 1-367 <SOU>
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RESULT 4
S51648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: tumor-suppressor protein p53 C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: S51648 R;Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R submitted to the EMBL Data Library, September 1994 submitted to the EMBL Data Library, September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741 (;Superfamily: cellular tumor antigen p53 (;Superfamily: cellular tumor antigen p53 (;Keywords: apoptosis; cell division control; DNA binding; homotetramer; F;161,164,224,280/Binding site: zinc (Cys, His, Cys, Cys) #status predict F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-386 < DEQ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cellular tumor antigen p53 - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S51648
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MNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTK
                                                     G-LAPPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGG
                                                                                             GQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGG
                                                                                                                                                PSLNKLFCQLAKTCPVQLWVDSPPPPGTRVRAMAIYKKLEHMTEVVRRCPHHERSSDYSD
                                                                                                                                                                                                TELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNE
                                                                                                                                                                                                                                                EPSAPAAPPPAT----PAPATSWPLSSFVPSQKTYPGNYGFRLGFLQSGTAKSVTCTYS
                                                                                                                                                                                                                                                                                            ---SPYAQPSSTFDALSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 744; DB 1;
Pred. No. 3.4e-44;
5; Mismatches 120
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A; Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2 C; Superfamily: cellular tumor antigen p53 C; Superfamily: cellular tumor antigen p53 C; Septens: apoptosis; cell division control; DNA binding; homotetramer; nuc F; 174, 177, 236, 240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F; 390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
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A;Title: Structure of the rat p53 tumor suppressor gene. A;Reference number: S41149; MUID:93181268; PMID:8441680
A;Accession: S41149
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A;Title: Nucleotide sequence of a CDNA encoding the rat A;Reference number: S02192; MUID:89083585; PMID:3060862
A;Accession: S02192
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A;Note: the nucleotide sequence was submitted to the EMBL C;Genetics:
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A; Residues: 1-173, 'W', 175-391 <HUL>
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A; Residues: 1-391 <SOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNLGLLNSMDQ------QIQNGSSSTSPYNTDHAQNSYT-APSPYAQPSSTFDALSPS
    NSSPPLNK - - - MNSMNKLPSVSQL
                                          FTLKIRGRERFEMFRELNEALELK----
                                                                          LYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSYG
                                                                                                                  VRVCACPGRDRRTEEENFRKKEEHCPELPPGSAKRALPTST----SSSPQQKKKPLDGEY
                                                                                                                                                       ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDEL
                                                                                                                                                                                             FRHSVVVPYEPPEVGSDYTTIHYKYMCNSSCMGGMNRRPILTITLEDSSGNLLGRDSFE
                                                                                                                                                                                                                                                                          TRVRAMAIYKKSQHMTEVVRRCPHHE----RCSDGDGLAPPQHLIRVEGNPYAEYLDDRQT
                                                                                                                                                                                                                                                                                                              AVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEGNSHAQYVEDPIT
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Pred. No. 9.8e-43;
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                                                                                                                                                                   cellular tumor antigen p53 [validated] - human
N;Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformati
C;Species: Homo sapiens (man)
C;Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C;Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397;
4905; I5854; I78850; I52681; S60153
A;Cross-references: EMBL:X01405; R;Buchman, V.L.; Chumakov, P.M.;
                                      A; Molecule type: DNA
A; Residues: 1-393 <LAM>
                                                                        A;Title: Characterization of A;Reference number: A25224; A;Accession: A25224
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A; Gene: p53
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A; Cross-references: GB:M75144; NID:g191414;
A; Experimental source: kidney, strain MP1
                                                                                                                                                       R; Lamb,
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Best Local :
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                                                                                                                                                       P.; Crawford, L
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                                                                                                                                     Biol. 6, 1379-1385, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.9%;
                                                                                              f the human p53 MUID:87064416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987 Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                              gene.
PMID:2946935
                                                                                                                                                                                                                                                                                                                                                                         353
                                                                                                                                                                                                                                                    oncoprotein p53; transformation
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N;Alternate names: tumor suppressor protein p53
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_char
C;Accession: JH0633
R;Legros, Y; McIntyre, P; Soussi, T.
Gene 112, 247-250, 1992
A;Title: The cDNA cloning and immunological characterization
A;Reference number: JH0633; MUID:92210007; PMID:1555773
A;Accession: JH0633
A;Accession: JH0633
                                                                                                                                                                                                                         C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nuc F;179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                       LYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSST
                                                                                                                                            Score 712; DB 1; Length 396; Pred. No. 5.8e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN: AAA37085.1;
                                                                                                                 110;
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92
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MTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQY 181
                                                                                                                                                                                                                                                                                                                                                                                       FDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKV 121
                                                    GRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS
                                                                                                                                                                                                                                                                                                                                                           PWPLSSS--VPSYKTYQGDYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQLAKTCPVQLWV
GRNSFEVRICACPGRDRRTEEKNFQKKGEPCPELPPKSAKRALPTNT---SSSPQPKRKT
                                                                                                                  LDDKQTFRHSVVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDPSGNLL
                                                                                                                                                                                                                                        SSTPPPGTRVRAMAIYKKLQYMTEVVRRCPHHERSSE-GDG-LAPPQHLIRVEGNMHAEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AGWLEDPGEALQGSAAAAAPAAPAAEDPVAETPAPVASAPAT
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rddns

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A;Molecule type: mRNA
A;Residues: 1-71, p',3-272,'H',274-393 <HAR>
A;Reference clone pR4-2, cell line A431
R;Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, Mol. Cell. Biol. 6, 4650-4656, 1986
A;Title: Molecular basis for heterogeneity of the human p53 protein.
A;Reference number: A93086; MUID:87089826; pMID:3025664
A;Accession: A25397
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A;Residues: 1-71,'p',73-93 <ZAK>
A;Residues: 1-71,'p',73-93 <ZAK>
A;Residues: 1-71,'p',73-93 <ZAK>
A;Residues: 1-71,'p',73-93 <ZAK>
A;Residues: 1-71,'p',73-93 <ZAK-
A;Residues: 1-71,'p',73-93 <ZAK-
A;References: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210
R;Harlow, E; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
A;Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular
A;Reference number: A55060; MUID:85267676; PMID:3894933
A;Accession: A55060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 101-393 KKII>
A; Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1;
A; Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1;
R; Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M.
EMBO J. 4, 1251-1255, 1985
EMBO J. 4, 1251-1255, 1985
A; Title: Human p53 cellular tumor antigen: cDNA sequence and e A; Reference number: A22837; MUID:85230577; PMID:4006916
A; Accession: A22837
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A; Residues: 1-71, 'P', 3-393 <BUC2>
A; Residues: 1-71, 'P', 3-393 <BUC2>
A; Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476
A; Note: this 72-Pro allele was found in both normal and malignant cell line
R; Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
submitted to the EMBL Data Library, August 1990
                                                                                                                                                            A; Molecule type: mRNA; DNA
A; Residues: 66-71, 'P',73-79 <MKI2>
A; Experimental source: clone lambda Cll3
A; Note: 72-Cys was also found, and appear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 3, 3257-3262, 1984
A;Title: Isolation and characterization of a human p53 cDNA clone: expression of A;Reference number: $42669; MUID:85128934; PMID:6396087
A; Experimental source: clone R; Farrell, P.J.; Allan, G.J.;
                                                                  A; Molecule type: mRNA; DNA
A; Residues: 66-79 < MKI3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-78,'T',80-393 <HAR1>
A;Residues: 1-78,'T',80-393 <HAR1>
A;Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A;Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
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A;Note: this 72-Arg allele appears to be about 5
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A; Accession: S40773
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A; Residues: 1-393 <BUC1>
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P.J.; Allan, G.J.;
                                                                                                                                    S42453
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                               J6K
   Shanahan,
                                                                                                                                                               appears
F.; Vousden,
                                                                                                                                                                   represent
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К.н.;
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   Crook,
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L.; Benchimol,
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Nucleic Acids Res. 19, 6977, 1991

A,Title: An Alu polymorphism intragenic to the TP53 gene A;Reference number: I38093; MUID:92107726; PMID:1762941 A;Accession: I38093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-247,'Q',249-393 <F08>
A; Cross-references: EMBL:X60017; NID:g506446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A; Cross-references: EMBL: X60016; NID: g506444;
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A;Residues: 1-189, 'LLSILSEWKEICVWSIWMTETLFDIVWWCPMSRLRLALT', 'VPPSTTTTCVTVPAWAA'
A;Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
A;Note: deletion of a C nucleotide causes a frameshift at position 566
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-253, 'D', 255-393 <F11>
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A; Residues: 1-71,'P',73-162,'H',164-393 <F09>
A; Cross-references: EMBL:X60018; NID:g506448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-247, 'Q', 249-393 <F06>
A; Cross-references: EMBL: X60015; NID: g506442;
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A; Residues: 1-245, 'T', 247-393 <F04>
A; Cross-references: EMBL: X60013; NID: g506438;
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A; Residues: 1-192, 'R', 194-393 < F02>
A; Cross-references: EMBL: X60011; NID: g506434;
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A;Title: p53 is frequently mutated in Burkitt's lymphoma cell lines. A;Reference number: 138082; MUID:92007731; PMID:1915267
A;Accession: 138082
                     A;Cross-references: EMBL:X54
R;Yamada, Y.; Yoshida, T.; H
Cancer Res. 51, 5800-5805, 1
A;Title: p53 gene mutations
                                                                                                                                                                                                                                                                                                                                                   A; Note: all sequences submitted to the EMBL/GenBank/DDBJ R; Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
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A; Residues: 1-236, 'I', 238-393 <F05>
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A; Residues: 1-393 <F03>
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A; Residues: 1-212,'Q',214-393 <F10>
A; Cross-references: EMBL:X60019; NID:g506450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: translated from GB/EMBL/DDBJ
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gene mutations in gastric cancer metastases
number: A44905; MUID:92034678; PMID:1933850
                                                                                                                                            1-393 <FUT>
                                             ces: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214 oshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, 5800-5805, 1991
                                                                                                                                                                           DNA
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A; Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBIP:63158)
A; Note: mutation from a liver metastasis of a gastric cancer R; Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L. Oncogene 6, 1067-1071, 1991
A; Title: Trac of the control of the control of the control oncogene control of the control of the control oncogene control of the control of the control oncogene control of the control of the control of the control of the control oncogene control of the control
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A; Molecule type: mRNA
A; Residues: 327-331, 'OgrsFQKENC' <CHO>
A; Residues: 327-331, 'OgrsFQKENC' <CHO>
A; Residues: 327-331, 'OgrsFQKENC' <CHO>
A; Roote: mutant sequence with altered splicing and termination expressed in Mo
R; Petersen, G; Song, D,; Huegle-Doerr, B; Oldenburg, I; Bautz, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1995
A; Title: Mapping of linear epitopes recognized by monoclonal antibodies with
A; Reference number: S60151; MUID:96133682; PMID:8552047
A; Accession: S60151
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A;Residues: 3-44 <PET>
R;Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
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A; Residues: 274-277, /S', 279-282 <HEN2>
A; Residues: 274-277, /S', 279-282 <HEN2>
A; Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1;
R; Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
A; Title: Alternative splicing of the p53 tumor suppressor general companies.
A; Reference number: 152681; MUID:94036762; PMID:8221626
A; Accession: 152681
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A;Cross-references: GB:S41969; NID:g1679931; PIDN:AAB19324.1;
A;Accession: I78850
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A; Molecule type:
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R;Bienz, b.,
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C:Blular tumor antigen p53 - mouse
R:Alternate names: oncoprotein p53
C;Species: Mus musculus (house mouse)
C:Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change
C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48
C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48
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Nucleic Acids Res. 17, 8375, 1989
A;Title: Nucleotide sequence of a cDNA encoding the monkey
A;Reference number: S06594; MUID:90045967; PMID:2530498
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S06594
A;Molecule type: mRNA
A;Residues: 1-159,'H',161-167,'G',169-233,'I',235-390
A;Residues: 1-159,'H',161-167,'G',169-233,'I',235-390
A;Croos-references: GB:X01237; GB:K01700; NID:953575
R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E
                                                                                       Nature 306, 594-597, 1983
A;Title: A single gene and a
A;Reference number: A02684; M
A;Accession: A02684
                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-134, 'V', 136-390 <CHU>
                                                                                                                                                                                                                                                                        A; Title: Primary structure of DNA complementary to murine A; Reference number: S06336; MUID:88221682; PMID:3329909 A; Accession: S06336
                                                                                                                                                                                                                                                                                                                                          R; Chumakov, P.M.
Bioorg. Khim. 13, 1691-1694, 1987
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-134, 'V', 136-390 <BIE>
A; Cross-references: GB: X00876; NID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
EMBO J. 3, 2179-2183, 1984
A;Title: Analysis of the gene coding for the murine cellular
A;Reference number: A22739; MUID:85027173; PMID:6092064
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A; Residues: 1-393 < RIG>
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                                                                                                                                                                                 R; Zakut-Houri, R.; Oren, M.;
                                                                                                                                                                                                                                                   A; Status: not compared with conceptual
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                                                                                                                 MUID:84068204;
                                                                                                                                                                                 Bienz,
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1; Mismatches
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Pred. No. 2.4e-41;
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PMID:6646235
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F;267-283/Region: conserved region V
F;313-319/Region: nuclear location signal
F;319-357/Region: tetramer association
F;7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F;389/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted
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A,Status: translated from GB/EMBL/DDBJ
A;Residues: 1-47, 'R',49-78, 'QW',82-390 <RES>
A;Residues: 1-47, 'R',49-78, 'QW',82-390 <RES>
A;Cross references: EMBL:X00741; NID:953570; PIDN:CAA25323.1; PID:953571
C;Comment: This DNA-binding protein plays an essential role in the regula C;Comment: The tetramer association region may exhibit a beta-turn, beta-C;Comment: The tetramer association region may exhibit a beta-turn, beta-C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; F;1-44/Domain: transcription activation #status predicted <TRA>
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A; Molecule type: mRNA
A; Residues: 1-167, 'G; 169-390 <ARA3>
A; Residues: 1-167, 'G; 169-390 <ARA3>
A; Cross references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1;
A; Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
Nucleic Acids Res. 12, 5609-5626, 1984
A; Title: Cloning and expression analysis of full length mouse cap: Reference number: 148703; MUID:84272240; PMID:6379601
A; Accession: 148703
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F;108-121/Region: L1 loop
F;114-139/Region: conserved region II
F;160-192/Region: L2 loop
F;168-178/Region: conserved region III
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R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.;
submitted to the EMBL Data Library, July 1988
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A; Residues: 1-167, 'G', 169-233, 'I', 235-390
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Best Local Similarity
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QHTIE-
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                                                                                               KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
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43.2%; Pred. No. 2.8e-41;
tive 54; Mismatches 97
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C; Superfamily: C; Keywords: li
                                                                                                                                                                              Gene 184, 177-183, 1997
A;Title: Cloning and characterization of Chinese hamster A;Reference number: JC6176; MUID:97183659; PMID:9031625
A;Contents: liver
                                                                                                                                                                                                                                                                           tumor suppressor protein p53 - Chinese hamster C;Speckes: Cricetulus griseus (Chinese hamster) C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 C;Accession: JC6176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: p53
C;Superfamily: cellular
C;Keywords: tumor
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A;Title: cDNA cloning and immunological characterization A;Reference number: JC6193; MUID:97208869; PMID:9055811 A;Accession: JC6193
                                     A; Gene: p53
                                                                                         A;Cross-references: GB:U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230 C;Comment: This protein is a multimer, it plays the central role in a complex DNA
                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-393 <LEE>
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997
C;Accession: JC6193
                                                        C; Genetics:
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A; Residues: 1-391 <LEA>
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Best Local
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                                                                                                                                                                                                                                           H.; Larner, J.M.; Hamlin,
84, 177-183, 1997
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                                                                           recombination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               QMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAPALAAPAPATSWPLSSSVPSQKTYHGNYGFRLGFLHSGTAKSVTCTYSPCLNKLFCQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TFDAL-SPSPA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLEDSSGNLLGRNSFEVRVCACPGRDRRTEEENFRKKGEPCPELPPGSSKRALPTTT--T
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                  cellular tumor
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                    antigen p53
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                                                                                                                                                                                                                                                            J.L.
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Pred. No. 3.9e-41;
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                                                                          interactions
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                                                                                                                                                                                                                                                                                                #text_change 23-Jul-1999
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A;Molecule type: mRNA
A;Residues: 1-381 <HANN
A;Residues: 1-381 <HANN
A;Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
A;Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
C;Comment: This sequence, produced by alternative splicing of the tenth intron, lacks to some known.
C;Superfamily: cellular tumor antigen p53
C;Superfamily: cellular tumor antigen p53
C;Keyvords: alternative splicing; phosphoprotein; zinc
C;I-44/Domain: transcription activation #status predicted <TRA>
F;16-56/Region: conserved region I
F;99-289/Domain: DNA-binding core #status predicted <DBC>
F;108-121/Region: Conserved region II
F;99-289/Domain: L1 loop
F;16-139/Region: conserved region IV
F;313-252/Region: conserved region IV
F;313-252/Region: conserved region V
F;313-319/Region: conserved region V
F;313-319/Region: conserved region Signal
F;319-357/Region: tetramer association
F;7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) #status predicted
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A; Accession: S38824
A; Molecule + ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cellular tumor antigen p53, minor splice form - mouse (;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999 C;Accession: S38824; S35478 R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, Mol. Cell. Biol. 6, 3232-3239, 1986 N;Title: Immunologically distinct p53 molecules generated by alternative spl. A;Reference number: S38822; MUID:87064640; PMID:3023970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200202 R;Han, K.A.; Kulesz-Martin, M.F.
Nucleic Acids Res. 20, 1979-1981, 1992
A;Title: Alternatively spliced p53 RNA in transformed and normal cells A;Reference number: S35478; MUID:g2253421; PMID:1579500
A;Accession: S35478
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Best Local S
Matches 143
;313-319/Region: nuclear location signal
;319-357/Region: tetramer association
;319-357/Region: tetramer association
;719,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
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Residues: 1-381 <ARA>
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47.2%; Prof
ative 52;
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Pred. No. 5.9e-41;
2; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation not
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A; Gene: p53
A; Introns: 24/1
C; Superfamily:
    A; Reference n
A; Accession:
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T19361
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         o the EMBL Data number: Z19114 : T19361
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hypothetical protein C17G1.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc.Accession: T19361 R;White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The canine p53 gene is subject to somatic in A;Reference number: I46226; MUID:95150524; PMID:784' A;Accession: I46226 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-77 <- ZEV > A;Cross-references: GB:L27630; NID:g508454; PIDN:AAO A;Cross-references: GB:L27630; PIDN:AAO A;C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cellular tumor antigen p53 - dog (fragment)
(;Speciles: Canis lupus familiaris (dog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
C;Accession: I46226
R;Devilee, P; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, Anticancer Res. 14, 2039-2046, 1994
A;Title: The canine p53 gene is subject to somatic mutations in thypoid carcinoma.
A;Reference number: I46226; MUID:95150524; PMID:7847847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 KAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEP
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|:||:||:||:|||
PEVGFDYTTIHYNYMCNS
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||| | ||:|:|||||:|:
UMCTYSPPLNKLFFQLAKTCPVQLWYSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHE- 177
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Pred. No. 1.7e-11;
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Pred. No. 2.4
August 1996
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A;Experimental source: embryo C;Genetics:
A;Gene: dri
                                                                                                                  R;Gregory, S.L.; Kortschak, R.D.; Kalionis, B.; Saint, R. Mol. Cell. Biol. 16, 792-799, 1996
A;Title: Characterization of the dead ringer gene identifies A;Reference number: JC6093; MUID:96182081; PMID:8622680
A;Accession: JC6093
                                                                                                                                                                                                                                      RESULT 15
JC6093
Gead ringer nuclear protein - fruit fly (Drosophila melanogaster)
G:Species: Drosophila melanogaster
C:Species: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
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A;Introns: 40/3; 98/2; 295/1; 443/3; 590/3; 619/3; 691/1; 810/1; 868/3
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology.
                                                                                     A; Molecule type: mRNA
A; Residues: 1-901 <GRE>
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A;Molecule type: DNA
A;Residues: 1-925 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 AVPIRHSPSQMPTHLQSPVHPSPNGAPPA-YNAPSSSKT-PDPTQQQRPHS--PTFAVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPSSRGSMDQRQLQQQQIQMQQY-HQH----MQMQKMQQQQMAAQQQMSRMGGSGPSSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPAAATLAQAFSANQISTK-PKTSPQKKKHEDGVPEPPTADTPFTTVTHYELPAAMTFLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAKSATWTYSTELKKLYCQIAKTCPIQIK----VMTPP----PQGAVIR-----AMPVYK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNQNNLLSPNHGASSLGSQKQHGSSPMGSSLMPLNGQYPSMTQNMQSPASTSMEPTFKEP
                                                                                                                                                                                                                                                                                                                                                                                                                          VSFLARLGCSSCLDYFTTQGLTTIYQIEH 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANHMGGMQPMNGTPTEGPTVNNIGLNSNNAAGLPPLSLRSQGPDGSQNNDFPGIPSTSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAEHV----TEVVKRCPNHELSREFNEGQIAPPSHLIRVEG-NSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGDMNGLSPTQALP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGGSQLPSLSAPSLQRADSMPQLPSQQQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-----SSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQXQTSI---QSPSSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYFDPK-----YNRM-----
                                                                                                                                                                                                                                                                                                                                                                                       -SNQAHALCAGC-HHFIMPGSSTLSCLYH 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SQSMHTPMISPNFNAS------QPSTSGRQ--PAKKARSASDASEPPFNVPH
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                                                                 NID:g1480739; PIDN:AAB05771.1; PID:g1480740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 152.5; DE Pred. No. 0.014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                    CLDYFTTQGLTTIYQ----IEHYSM----DDLASLKIPE-QFRHAIWKGILDHRQLHEFSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                         EGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE-----PPQV-------G
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QQMNGHHHHQTHHLDKSDDSAIENSPTTSTTTGGSV
                             S----
                                                       ---YLNPHNMAAVAAAAGFHHPSMGHQQDAASEGEPEDDYAHGEHNTTGNSSSMHDDSEP
                                                                                                                                                                                                                                                                                                                                                                                TEFTTVLYNFMCNS-----SCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICAC
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                                                                                                                 TNIKREREPTPEPVDQDDKFVDQPPPAKRVGSG--LLPPGFPANF
                                                                                                                                             ANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSS
                                                                                                                                                                          HLQQQRQRSQSPDLSKHEALSAQVALWHMYHNNNSPPGSAHTSPQQREALNLSDSPPNL-
                                                                                                                                                                                                                                                               RETYEMLLKIKESLELMQYLPQHTI------ETYRQQQQQQQHQHLLQKQTSIQ--
                                                                                                                                                                                                                                                                                             AAHHRLMGAPAFG - -
                                                                                                                                                                                                                                                                                                                         PGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRG
                                                                                                                                                                                                                                                                                                                                                   RRSSYGQYEAMHNQMPMTPISRPSLPGGMQQMSPLALVT----HAAVANNQQAQAAAAAA
                                                                                                                                                                                                    --SPSSYGNSSPPLNKMNSM------NKLPSVSQLINPQQRNALTPTTIPDGMG
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Pred. No. 0.24;
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2003, 09:53:28

Search completed: 7 Job time: 20.4749 August 9 secs

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Listing first 45 summaries
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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    SwissProt_41:*
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Copyright (c) 1993 - 2003
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P73_CERAE
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    P53_CANFA
P53_MARMO
P53_MARMO
P53_ORYLA
P53_SHEEP
P53_CAVPO
P53_TUPGB
P53_TLAFE
P53_SPBE
P53_SPBE
P53_CERAE
P53_MACFA
P53_MACF
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P53_CHICK
P53_FELCA
P53_TETMU
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P53_XENLA
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SEQUENCE FROM N.A. (ISOFORMS GAMMA TISSUE=Neuroblastoma; MEDLINE=9902167; PubMed=9802988; De Laurenzi V., Costanzo A., Barca Annicchiarico-Petruzzelli M., Levra Transcriptional activity.", J. Exp. Med. 188:1763-1768(1998). [5] SEQUENCE FROM N.A. (ISOFORMS EPSII TISSUE=Breast cancer, Hepatoma, Ly MEDLINE=99310938; PubMed=10381646]. De Laurenzi V., Catani M.V., Terri Costanzo A., Levrero M., Knight R. "Additional complexity in p73: Ind and identification of two new spli	SEQUENCE FROM N.A. (ISOFORM ALPHA). MEDLINE-9289209; PubMed=10362363; YOShikawa H., Nagashima M., Khan M.A Harris C.C.; "Mutational analysis of p73 and p53 Oncogene 18:3415-3421(1999). [3] SEQUENCE FROM N.A. (ISOFORM ALPHA). MEDLINE-98389621; PubMed=9721206; Mai M., Huang H., Reed C., Qian C., Jenkins R., Smith D.I., Liu W.; "Genomic organization and mutation a oligodendrogliomas with chromosome 1 Genomics 51:359-363(1998).	HUMAN CT-200 CT-200 CT-200 CT-200 CT-200 CP-70 OR P7 OR P7 TAXID ENCE FI ENCE FI LINE-901 AN A	134.5 133.5 133.5 133.5 129.5 129.5 129.5 129.5 129.5 128.5 128.5 128.5
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"Solution structure of a conserved C-terminal domain estructural homology to the SAM domain.";

EMBO J. 18:4438-4445(1999).

-I-FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SI
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Kharbanda S.,
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MEDLINE=99318135; PubMed=10391251;
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                                    TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER, SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
INDUCTION: NOT INDUCED BY DNA DAMAGE.
INDUCTION: NOT INDUCED BY DNA DAMAGE.
DOMAIN: POSSESS AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SIA DOMAIN.
TO THE ABL TYROSINE KINASE SIA DOMAIN.
DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRACT TO P53. HEMIZYGOSITY IS OBSERVED IN HUMAN CANCERS, IN CONTRACT TO P53. HEMIZYGOSITY IS OBSERVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN.

SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS

TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HO

AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM

AND HITH P53, WHEREAS ISOFORM FITH ALL P73 ISOFORMS. IS

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INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALI
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NEUROBLASTOMA
SIMILARITY: BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Epsilon;
IsoId=O15350-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SÜBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
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atl. Cancer Inst. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=015350-3; Sequence=VSP_006540, wote=The splicing of exon 11 results original reading frame;
                                                                                                                                                                                                                                                                                 IsoId=015350-7;
                                                                                                                                                                                                                                                                                                                                                                             Note=The splicing original reading 1 reading frame to 1
                                                                                                                                                                                                                                                                                                                                IsoId=015350-6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=015350-1; Sequence=Displayed;
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399:814-817(1999).
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., Weichselbaum
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, Weichselbaum
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BELONGS
                          AND OLIGODENDROGLIOMA
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                                                                                                                                                                                                                                                                                                                              Sequence=VSP_006546;
                                                                                                                                                                                                                                                                                                                                                                             sequence=VSP_006544, VSP_006:
ng of exon 11 results in a fra
frame. The splicing of exon
the sequence of isoform Alph
                                                                                                                                                                                                                                                                            Sequence=VSP_006538;
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pfam; pF00536; SAM; 1.
pRINTS; pR00386; p53SUpPRESSR.
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                                                                                                                                                                                                                              GO; GO:0003700; F:transcription factor activity; TAS. GO; GO:0008630; P:induction of apoptosis by DNA damage; GO; GO:0006298; P:mismatch repair; TAS. InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                          Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                             3D-structure.
                                                                                                                                                     Apoptosis; Nuclear
                                                                                                                                                                                                                                                                                   TRANSFAC; T04931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y11416; CAA72220.
Y11416; CAA72221.
Y11416; CAA72219.
                                                                                                                                                                                                                                                                                                                    AF079093;
                                                                                                                                                                                                                                                                                                            AL136528;
                                                                                                                                                                                                                                                                                                                                                                                                                       AF079094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AF077625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF077621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF077619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF077618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF077617;
                                                                                                                                                                               SM00454;
                                                                                                                                                                                                                                                                         HGNC:12003; TP73.
                                                                                                                                                                                                                                                                                          08-AUG-01.
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287
346
346
168
391
483
131
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                                                                                                                                                                              SAM;
                                                                                                                                                                                                                                                                                                                                                                                                     AAD39696.
                                                                                                                                                                                                                                                                                                            CAB92742
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                                                                 46
304
435
171
171
394
486
486
310
                                                                                                                                                     protein;
                        636
                                                                                                                                                     Activator; DNA-binding; Anti-or n; Phosphorylation; Alternative
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             isoform Kappa).
/FTIG-VSP_006538.
SFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPE
QYRMTIWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGE
                                                         BETA
                                                                  PHOSPHORYLATION
                                                                          DNA-BINDING
                                                                                   POLY-PRO
                                                                                                   POLY-PRO
                                                                                                            MEDIATES OLIGOMERIZATION
                                                                                                                   ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                    TRANSACTIVATION (BY SIMILARITY).
       LQRQRVMEAVHFRVRHTITIPNRGGPGGGPDEWADFGFDLP
                                               GNTRCRHWVLCGDRGLSRPVLQGPSG
                                                                (POTENTIAL).
                                                                ABL)
                                                                                                                                                             Anti-oncogene;
                                                                  (IN ISOFORM
                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                   TAS
                                                                                                                                                     splicing;
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P73_CERA2
P73_CERA2
ID P73_C
AC 09XSK
DT 16-0C
DT 16-0C
DT 28-FE
GN TP73.
Cerco
OC Cerco
OC Eukar
OC Mamma
OC NCBI-
CO TISSU
RN [1]
RP SEQUE
RA Caput
RA Submit
CC -!- F
CC -!- T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 346
                                                                                                                                                                                                                                                                     protein).
TP73 OR F
                                                                                                                                                                                               Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalla; Butherla; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                          Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
--I- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROJ
                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor protein p73 (p53-like transcription factor)
                                                                                                                                                                                                                                                                                                                                                             P73_CERAE
Q9XSK8; Q9TSQ9;
                                                                                                                                         TISSUE-Kidney;
                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                       NCBI_TaxID=9534;
(BY SIMILARITY).
SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO TYROSINE KINESE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOT AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
                                                                                                                                                                                                                                                                     OR P73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSV-GSSETRGERVIDAVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLFTTYQIEHYSMDDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMNKLPSVNQLVGQPPPHSSAATPNLGPVGPG----MLNNHGHAVPANGEMSSSHSAQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMNKLPSVSQLIN--PQQRNALTPTTIPDGMGANIPMMGTH---MPMAGDMNGLSPTQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--TSIKKRRSPDDELLYLPVRGRETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDRKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVRGRENF
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                                                                                                                                                        N.A.
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                        (ISOFORMS
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59.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1741; DB 1;
Pred. No. 5.7e-112;
                                                                                                                                                        ALPHA
                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                        AND
                                                                                                                                                                                                                                                                                                                                                                             637
                                                                                                                                                        BETA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       629
                                                                                                                                                                                                                                    Euteleostomi;
              HOMOTYPICALLY
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Matches 340
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EMBL; Y11419;
HSSP; O15350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation;
Apoptosis; Nuclear proteir
VARSPLIC 495 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001660; S
Pfam; PF00870; P53; 1.
Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS: Event-Alternative splicing; Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO THE ABL TYROSINE KINASE SH3 DOMAIN. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOId=Q9XSK8-2; Sequence=VSP_006537;
DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLICOMERIZATION DOMAIN THAT BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a casen the Swiss Institute of Bioinformatics and the EMBL
              420
                                                                            366
                                                                                                                                        306
                                                                                                                                                                                                                                                                  186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        LLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTEDALSPSPAIPSNTDYPGPH
                                                                                                                                                                                                                    GTEFTTVLYNFMCNSSCYGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKAD
                                                                                                                                                                                                                                                                                HVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQV
                                                                                                                                                                                                                                                                                                                                           SFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAE
                                                                                                                                                                                                                                                                                                                                                                                        GVNKLPSVNQLVGQPPPHSSAATPNLGPVGSG---
                                           SMNKLPSVSQLIN--PQQRNALTPTTIPDGMGANIPMMGTH---MPMAGDMNGLSPTQAL
                                                                                          EMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMN-
                                                                                                                                                           EDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--TSIKKRRSPDDELLYLPVRGRETY
                                                                                                                                                                                                    GTEFTTILYNFMCNSSCVGGMNRRPILIIITLETRDGQVLGRRSFEGRICACPGRDRKAD
                                                                                                                                                                                                                                                                  HVTDIVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQV
                                                                                                                                                                                                                                                                                                                              HFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSAPPPPGTAIRAMPVYKKAE
                                                                                                                           EDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGPGVKKRRHGDEDTYYLQVRGRENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002117; P53.
IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAA72224.1; -. CAA72225.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activator; DNA-binding; Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation: Alternative splicing.
SELTGLGCTNCIEVETSQGLQSIYHLQNLTHIBLGALKIPE
OYRMTIWRGLQDLKQGHDYGAAAQQLLRSSNAAAISIGGSG
ELQRQRVMEAVHFEVRHTITIPNRGGFGAGFDEWADFGFDL
PDCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1720.5;
Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP_006537.
7CB200B919C9C70A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..5e-110;
les 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                -MLNNHGHAVPANSEMTSSHGTQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
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L outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Query Match
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28-FEB-2003 (Rel. 41, Last
Cellular tumor antigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P53_ONCMY P25035;
                                                                                                                                                                                                                                                                                                                                                                                             PIR; JH0631; JH0631.
HSSP; P04637; ITUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE=92210006; PubMed=1339362; de Fromentel C.C., Padkel F., Chapus "Rainbow trout p53: cDNA cloning and Gene 112:241-245(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use
                                                          SEQUENCE
                                                                                                                                           DOMAIN
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                DNA_BIND
                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                    Nuclear protein;
                                                                                                                                                                                                                                                                                                           ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities
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                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M75145; AAA49605.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes regulared for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffied and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                 _RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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369
303
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                                                                                                                                                                                                                                                                                    DNA-binding;
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                                                                                                                                   Phosphorylation; Apoptosis.

44 TRANSCRIPTION ACTIVATION (ACIDIC).

281 BY SIMILARITY.

356 OLIGOMERIZATION.

392 BASIC (REPRESSION OF DNA-BINDING).
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356
392
318
395
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                                                                                                                                                                                                                                                                              Transcription regulation; Activator;
                                                    BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
8422250765545A1C CRC64;
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     839.
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biochemical characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396
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Length 396;
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RESULT 4
P53_BARBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P53_BARBU
Q9W678;
16-OCT-2001
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;

"Evolutionary conservancy of p53 gene sequences in fish.";

"Evolutionary conservancy of p53 gene sequences in fish.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyprinidae; Barbus.
NCBI_TaxID=40830;
                                                                                        or send
                                                                                                                                                   between the Swiss Institute of Bioinfo
the European Bioinformatics Institute.
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellular tumor antigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinopterygii; Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barbus barbus (Barbel).
                                                                                                                                                                                                              expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                          AF071570;
P04637; 1T
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                                                                                       an email to license@isb-sib.ch).
                                                                                                                   non-profit institutions as long and this statement is not removed.
                                                                                                       requires a license agreement
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(Rel.
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                                                          AAD34212.1;
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. 40, Last sequ
. 41, Last anno
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Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 suppressor
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                                                                                                   (See http://www.isb-sib.ch/announce/
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                                                                                                                                                There are no
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Ostariophysi; Cypriniformes;
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                                                                                                                     Usage
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Pfam; PF00870; InterPro;

P53;

637; 1TUP. IPR002117;

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P53_BARE
P53_BARE
ID P53_B
AC P7973
DT 01-NO
DT 01-NO
DT 28-FE
DE CELTA
OC ACTION
OC CYPTI
CON CHIL
RN [1]
RP SEQUE
RX Cheng
RA Thong
CO -1-F
CC -1-F
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Best Local S
Matches 167
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DOMAIN 1
DABIND 66
DOMAIN 298
DOMAIN 342
DOMAIN 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P53_BRARE STANDARD; PKI; 3/3 FA.
P79734; Q90440;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                        Winge P.;
Submitted
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=97344388; PubMed=9200835;

Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,

Chongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;

"Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence expression during embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellular tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
SEQUENCE
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                                                                                                                                                                                                          SEQUENCE
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FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes regulared for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR DRP53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319
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167; Conser
                                                                                                                                                                                                          QF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLKKINDSLELSDVVPPSEMDRYRQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQVSDSTKNGD----GTKRPF-RQNTHGIQMTSIKKRR----SPDDELLYLPVRGRETYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRCPHHERTPD-GDG-LAPAAHLIRVEGNSRALYREDDVNSRHSVVVPYEVPQLGSEFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVV
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                                                                                                                                                                                                                                                      Biol.
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                                                                                                                                                                                                                                                 Biotechnol. 6:88-97(1997).
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51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p53
                                                                                                                                                   the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₹.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 819.5; DB 1
Pred. No. 4.1e-49;
9; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC (REPRESSION OF NUCLEAR LOCALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cion; Apoptosis.
TRANSCRIPTION ACTIVATION
BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBE2CF2CEA74C304 CRC64;
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LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369;
                                                                                                                                                                                                                                                                                                 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312
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SGREDACE

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(Rel. (Rel.

40, Created)

STANDARD;

PRT;

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Cellular tu TP53 OR P53

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40, Last sequence up 41, Last annotation tigen p53 (Tumor sup)

suppressor p53)

[ctalurus

punctatus (Channel catfish)

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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1. Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U60804; AAB40
EMBL; U46693; AAA97
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis induction seems to be mediated either by stimulation BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                            114
                                                                                                                                   234
                                                                                                                                                                                        174
                                                                                                                                                                                                                 108
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Pro; IPR002117; P53.
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                                                                                                                                                                                                                                                                                                                                                   ENNAQTQFSEPQYTNL------GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPS
                                                                                                                                                                           EGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTL
                                                                                                                                                                                                                                                                                    PYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAK
                                                                                                                                                                                                                                                                                                                         QNDSQ-EFAELWEKNLIIQPPGGGSCWDIIN--DEEYLPGS-----FDPNFFEN-VLEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long as its content and this statement is not removed. Usage by ar
                                                     LRPEGSKKAKGSSSDEEIFTLQVRGRERYEILKKLNDSLELSDVVPASDAEKYRQK
                                                                              M----TSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ
                                                                                                        ETQEGQLLGRRSFEVRVCACPGRDRKTEESNFKKDQETKTMAKTTTGTKRSLVKESSSAT
                                                                                                                     ETRDGQVLGRRCFEARICACPGRDRKADEDSIRK-QQVSDSTKNGDGTKRPFRQNTHGIQ
                                                                                                                                                              EGNQRANYREDNITLRHSVFVPYEAPQLGAEWTTVLLNYMCNSSCMGGMNRRPILTIITL
                                                                                                                                                                                                                 TCPVQMVVDVAPPQGSVVRATAIXKKSEHVAEVVRRCPHHE--RTPDGDNLAPAGHLIRV
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345
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373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation; Apoptosis.
31 TRANSCRIPTION ACTIVATION
260 BY SIMILARITY.
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332
366
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372
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48.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). PHOSPHORYLATION (BY SIMILARITY).

AC7AB724FA6B61FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                          Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            806.5;
No. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                            2e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulation;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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Matches
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-IF FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of expression (By similarity).

-I- SUBUNIT: Binds DNA as a homotetramer (By similarity).

-I- SUBCELLULAR LOCATION: Nuclear.

-I- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification and characterization of the channel catfish (Ictalurus punctatus)."; Comp. Biochem. Physiol. 120B:675-682(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send
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Luft J.C., Bengten E., Clem L.W., Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00870; P53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
  292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
ASKKSKNSSSDDEIYTLQVRGKERYEFLKKINDGLELSDVVPPADQEKYRQK 343
                                                                                                                              LETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQ
                                                                                                                                                                                              VEGNSRAVYQEDGNTQAHSVVVPYEPPQVGSQSTTVLYNYMCNSSCMGGMNRRPILTIIT
                                                                                                                                                                                                                                                                                             KTCPVLMAVSSSPPPGSVLRATAVYKRSEHVAEVVRRCPHHERSNDSSDGP-APPGHLLR
                                                                                                                                                                                                                                                                                                                            KTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                             SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA
                                              MTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 344
                                                                                                                                                                                                                                                 VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVT
                                                                                                                                                                                                                                                                                                                                                                                               SDMLQPQSS--SSPPTSTVPVTSDYPGLLNFTLHFQESSGTKSVTCTYSPDLNKLFCQLA
                                                                                               LETQDGHLLGRRTFEVRVCACPGRDRKTEESNFKKQQ-EPKTSGKTLTKRSMKDPPSHPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSCRIPTION ACTIVATION (ACIDIC) BY SIMILARITY. OLIGOMERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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PSSULT 7
PSS_XEMIT 7
PSS_XEMIT
                                                                                                                                                                                                                                                                                                                           EMBL; S68353; AAC60746.1; -
PIR; A29376; A29376.
HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                   MOD_RES
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P53_XENLA
P07193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Overexpression or miles in Xenopus laevis embryos.";
Oncogene 9:109-120(1994).
-!- FUNCTION: Acts as a tumor suppressor
                                                                                                                                                                                                                                                         PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M36962; AAA49923.1; -. EMBL; X05191; CAA28821.1; -. EMBL; X77546; CAA54672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression (By similarity).
-!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for a protein homologous to human and Oncogene 1:71-78(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellular tumor antigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1988
28-FEB-2003
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CONFLICT
                                                                                                                  DOMAIN
                                                                                                                                          DOMAIN
                                                                                                                                                                DNA_BIND
                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                           Nuclear protein;
                                                                                                                                                                                                                                 Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoever M., Clement J.H., Wedl
"Overexpression of wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata;
Amphibia; Batrachia; Anura; Mesobatrach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-94134403;
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"Cloning and characterization of a cDNA from Xenopus
for a protein homologous to human and murine p53.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88143684; PubMed=2830576;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
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                                                                                                                                                                                                         DNA-binding; Transc
n; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wedlich D., Montenarh M., Knoed type p53 interferes with normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update) annotation updat
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Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                 Transcription regulation;
  MISSING
                   PHOSPHORYLATION (BY SIMILARITY).
T -> S (IN REF. 2).
MISSING (IN REF. 2).
                                                                                         BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                             TRANSCRIPTION ACTIVATION BY SIMILARITY.
                                                                                                                                            OLIGOMERIZATION
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                                                                                                                                                                                                           Apoptosis
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NI ()
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                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                           Oncogene 18:5005-5009(1999).
                                                                                                                                                                                                                                                                                                                                                                             antibodies
                                                                                                                                                                                                                                                                                                                                                                                      Burr P.D., Argyle D.J., Reid S.W.J., "Nucleotide sequence of the porcine precombinant porcine p53 expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
Cellular tumor antiger
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99422034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
                                                                                                                                                                  expression.

SUBUNIT: Binds DNA as a homotetramer (By similarity).

SUBCELLULAR LOCATION: Nuclear.

DISEASE: p53 is found in increased amounts in a wide of transformed cells. p53 is frequently mutated or in
                                                                                                                                                                                                                                                         FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scrofa (Pig).
                                                                                                                                            SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                                                                              BAX and FAS antigen expression, or by repression
                                                                                                                                                         in many types of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR P53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128
    AF098067; AAF04620.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKRR---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRVCACPGRDRRTEEDNYTKKRGLKPSGK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRHSVCVPYEGPQVGTECTTVLYNYMCNSSCMGGMNRRPILTITLETPQGLLLGRRCFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYMEDVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCAVPSTDDYAGKYGLQLDFQQNGTAKSVTCTYSPELNKLFCQLAKTCPLLVRVESPPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=10490836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40692 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
in p53 (Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                    Reid S.W.J., Nasir L.;
the porcine p53 cDNA, and the detection
expressed in vitro with a variety of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 762; DB 1;
Pred. No. 3.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CE1F3E58F020D74D
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                                                                                                                                              FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELAHPPSSEPPLPKKRLVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                       wide variety or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                              of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                      of anti-p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                   of
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                                                                                                                                                                                                                                                                                                               RESULT 9
P53_CHICK
ID P53_CHICK
AC P10360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 156
                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel.
01-MAR-1989 (Rel.
28-FEB-2003 (Rel.
Nucleic Acids Res. 16:11383-11383(1988).
-i- FUNCTION: Acts as a tumor suppressor in many tumor types;
-growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regula a trans-activator that acts to negatively regulate cell di
                                                                       "Nucleotide sequence oncoprotein.";
                                                                                                                               STRAIN-SPAFAS
                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                         Cellular
                                                                                                                                                                                                                                                                                                    01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-oncogene; DNA-binding; Transcription r
Nuclear protein; Phosphorylation; Apoptosis
DOMAIN 1 45 TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 2.
PROSITE; PS00348; P53; 1.
                                                                                                   Soussi T
                                                                                                                MEDLINE=89083584;
                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                 Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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InterPro; IPR002117;
                                                                                                                                                                                                                                                                                                                                                                                                     338
                                                                                                                                                                                                                                                                                                                                                                                                                                 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 NSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGT
                                                                                                                                                                                                                                                                                                                                                                                                     NDALELKD-----AQTARESGENRAHSSHLKSKKG--QSPSRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLGFLHSGTAKSVTCTYSPALNKLFCQLAKTCPVQLWVSSPPPPGTRVRAMAIYKKSEYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHV
                                                                                                                                                                                                                                                                                                                                                                                                                                 KESLELMQYLPQHTIETYRQ--QQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFLKKGQSCPEPPPGSTKRALPTST---SSSPVQKKKPLDGEYFTLQIRGRERFEMFREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCTTIHYNFMCNSSCMGGMNRRPILTIITLEDASGNLLGRNSFEVRVCACPGRDRRTEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEVVRRCPHHERSSDYSDG-LAPPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYEPPEVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWLDENPDDASRVPAP-----PAATAPAPAPAPATSWPL--SSFVPSQKTYPGSYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386
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361
304
15
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                                                                                                                                                                                                   Aves;
                                                                                                                                            N.A.
                                                                                                                                                                                                                                                         antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                        10,
41,
                                                                                                                PubMed=3060861;
                                                                                                                                                                                                                                                                                                   10,
                                                                                                                                                                                                   Neognathae;
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349
380
316
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                                                                                    of a
                                                                                                                                                                                                                                                       , Last sequence of Last annotation en p53 (Tumor su)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                    cDNA encoding the chicken
                                                                                                                                                                                                                                                       sequence update)
annotation update)
(Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.1e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 761.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSCRIPTION ACTIVATION (ACIDIC) BY SIMILARITY.
                                                                                                                                                                                                                Craniata; Vertebrata;
                                                                                                                                                                                                   Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A4C3D88E8DF55162
                                                                                                                                                                                                                                                                                                                                367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
                                                                                                                                                                                                    Phasianidae;
                                                                                                                                                                                                                                                         p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
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                                                                                    p53
                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                 365
                                                                                                                                                                                                                                                                                                                                                                                                      373
    cell division
                                                                                    nuclear
              regulation
                                                                                                                                                                                                    Phasianinae;
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101

203

161

220

337

280

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P53_FELI
ID P5
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AC P4
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DT 28
DE Ce
GN TP
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OX NC
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Best Local
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                                                                                                                                              JLT 10
FELCA
                                                                                                       P53_FELCA
P41685;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                   TP53 OR TRP53
                                                                 Cellular tumor antigen
                                                                             01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                       Felis silvestris catus (Cat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S02193; S02193.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression (By similarity).
SUBUNIT: Binds DNA as a homot.
SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the activated genes is an inhibi
Apoptosis induction seems to be
BAX and FAS antigen expression,
                                                                                                                                                                                               291 PPTEAPEPPK-KRVLNPDNEIFYLQVRGRRRYEMLKEINEALQLAE
                                                                                                                                                                                                                                                                                                       178
                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X13057; CAA31456.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                                                       QNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQ
                                                                                                                                                                                                                                                                 SHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPI
                                                                                                                                                                                                                                                                                                                                                                     AAAAPPPLNPP--TPPRAAPSPVVPSTEDYGGDFDFRVGFVEAGTAKSVTCTYSPVLNKV
                                                                                                                                                                                                                                                                                                                                                                                                                          SVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKL
                                                                                                                                                                                                                                                   LTILTLEGPGGQLLGRRCFEVRVCACPGRDRKIEEENFRK-----RGGAGGVAKRAMS
                                                                                                                                                                                                                                                                                                     QHLIRVEGNPQARYHDDETTKRHSVVVPYEPPEVGSDCTTVLYNFMCNSSCMGGMNRRPI
                                                                                                                                                                                                                                                                                                                                                        YCRLAKPCPVQVRVGVAPPPGSSLRAVAVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002117;
                                                                          (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
308
347
292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,
                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation; Apoptosis:
30 TRANSCRIPTION ACTIVATION (ACIDIC)
278 BY SIMILARITY.
339 OLIGOMERIZATION.
              Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n set of ge
                           Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40169
                                                               p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                             (Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes required for this process. One of
an inhibitor of cyclin-dependent kinases
ms to be mediated either by stimulation
ression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 758.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY SIMILARITY). FC37D0FCDF9195B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                         Craniata;
                                                                                                                                 PRT;
             Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.1e-45;
ches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions on ng as its content is in no
             Vertebrata; Euteleostomi;
ia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                                               p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of.
                                                                                                                                                                                                                                                                            285
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                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D26608; 1
EMBL; D16460; 1
HSSP; P04637;
                                                                                                                                                                               MOD_RES
CONFLICT
                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷ :- '-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and chromosomal suppressor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okuda M., Umeda A., Matsumoto Y., Momoi
O'Brien S.J., Tsujimoto H., Hasegawa A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watari T., Goitsuka R., Tsujimoto H., He
"Cloning of feline p53 tumor-suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Lymph node; MEDLINE-94333960;
                                                                                                                                                                                                                                                                                                         Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94114699; PubMed-8286534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 34-354 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hematopoietic tumors."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okuda M., Umeda A.,
                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Int. J. Cancer 58:602-607(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                                                      Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression.

SUBUNIT: Binds DNA as a homotetramer (By similarity).

SUBCELLULAR LOCATION: Nuclear.

DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.

SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAX and FAS antigen expression, or by
                                                                                                          al Similarity
147; Conserv
                                                                               43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Med. Sci. 55:801-805(1993).
SVTCTYSPPLNKLFCQLAKTCPVQLWVRSPPPPGTCVRAMAIYKKSEFMTEVVRRCPHHE
                          SATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHE
                                                    DDASGMSAVPAPAAPAPAT----PAPAISWPLSSFVPSQKTYPGAYGFHLGFLQSGTAK
                                                                              DHAQNSVTAPSPYAQPSSTFDALSPSPAI-----PSNTDYPGPHSFDVSFQQSSTAK
                                                                                                                                                                                                                                                                                                                                                                                           IPR002117; P53.
                                                                                                                                                                 385
285
386 AA;
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318
361
304
                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   BAA05653.1;
BAA03927.1;
                                                                                                                                                                                                                                                                                                                                                                                                           10LG.
                                                                                                                                                                                                                                                                                           Phosphorylation; Apoptosis.

TRANSCRIPTION ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8056458;
., Sakai T., Ohashi T., Momoi Y.,
ka R., Tsujimoto H., Hasegawa A.;
                                                                                                                                                                               385
285
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349
380
316
                                                                                                                                                                 42692
                                                                                                                          49.88;
                                                                                                                                                                  ¥.
                                                                                                           49;
                                                                                                                                                                                                                                                                                                                     Transcription regulation; Activator;
                                                                                                                          Pred.
                                                                                                                                    Score 753.5;
                                                                                                                                                                               K -> R (IN REF.
                                                                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                     BASIC (REPRESSION OF NUCLEAR LOCALIZATION
                                                                                                                                                                                            PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                        PHOSPHORYLATION
                                                                                                                                                                                                                                                                  OLIGOMERIZATION
                                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                  D08B43BA1BC8EB78 CRC64;
                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mapping
                                                                                                                          No. 1.4e-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y., Watari T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repression
                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of feline
                                                                                                                                                                                                                     (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                        PRPK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             its aberration
                                                                                                                                                                                                                                      DNA-BINDING)
SIGNAL (POTE
                                                                                                           Indels
                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Youn H.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Bcl-2
                                                                                                                                                                                                                                                                                            (ACIDIC).
                                                                                                                                                                                                                        (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goitsuka
                                                                                                                                       386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor
                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                            17;
                                                                                                           Gaps
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 172
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PS3_TERMU ID PS3_T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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Q9W679;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, I
28-FEB-2003 (Rel. 41, I
                               DOMAIN
DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon miurus (Congo puffer).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                               HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Evolutionary conservancy of p53 gene sequences in fish.", Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bhaskaran A., May D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular tumor antigen
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF071571; AAD34213.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=94908;
                                                                                                                                        DNA_BIND
                                                                                                                                                                  DOMAIN
                                                                                                                                                                                               Nuclear
                                                                                                                                                                                                                                            ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                      Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression (By similarity).
SUBUNIT: BINGS DNA as a homotetramer (By
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155
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                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                        PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPGSTKRALPPST---SSTPPQKKKPLDGEYFTLQIRGRERFEMFRELNEALEL
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342
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                                                                                                                                                            Phosphorylation; Apoptosis.

Phase Transcription regulation; Activator;
                                                         273
337
363
301
     41266
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rand-Weaver M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Tumor suppressor p53).
                         BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE PHOSPHORYLATION (BY SIMILARITY).
                                                                                                               OLIGOMERIZATION
                                                                                                                                        TRANSCRIPTION ACTIVATION (ACIDIC) BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
  CRC64
                                                   SIGNAL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329
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RESULT 12
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Best Local S
Matches 148
                                                      Kraegel S.A., Pazi K.A., Madewell B.R.;

Sequence analysis of canine p53 in the region of exons 3-8.";

Sequence analysis of canine p53 in the region of exons 3-8.";

Cancer Lett. 92:181-186(1995).

-1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53_CANFA STANDARD; PRT; 381 AA. 029537; Q9TV78; 01-NOV-1997 (Rel. 35, Created). 15-DEC-1998 (Rel. 37, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor)
+ + +
                                                                                                                                                                                                                                     STRAIN=Beagle;
MEDLINE=95323915; PubMed=7600529;
                                                                                                                                                                                                                                                                                                                    Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka Watari T., Hasagawa A., Tsujimoto H.; "Aberrations of p53 tumor suppressor gene in various spontaneous tumors in the dog.";
                                                                                                                                                                                                                                                                                                                                                                                                                                Veldhoen N., Milner J.;
"Isolation of canine p53 cDNA and full length canine p53 protein.";
Oncogene 16:1077-1084(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Leukocyte;
MEDLINE=98178696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                        SEQUENCE OF 25-300 FROM
                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
              SUBUNIT: Binds DNA as SUBCELLULAR LOCATION:
                                            expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKSKTASSAEEDNNEVYTLQIRGRKRYEMLKKINDGLDLLENKPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN
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p53 is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9519881;
 found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                                      the EMBL/GenBank/DDBJ
              a homotetramer (By similarity). Nuclear.
'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
increased amounts in a wide variety
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RESULT 13
P53_BOVIN
ID P53_B
AC Q2962
DT 01-NO
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Best Local Similarity
Matches 159; Conserv
P53_BOVIN
Q29628;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF060514; AACLDYUY...
EMBL; AB020761; BAA78379.1
EMBL; S77819; AAB42022.1;
EMBL; B04637; 10LG.
HSSP; P04637; 10LG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodom; PD002681; P53; PROSITE; PS00348; P53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00386; P53SUPPRESSR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.
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                                                                                                                                                                                                                                                      YYEDPITGRQSYLVPYEPPQYGTEFTTYLYNFMCNSSCYGGMNRRPILLIYTLETRDGQV
                                                                                             KLMFKREGLDS
                                                                                                                    HLLQKQTSIQS 361
                                                                                                                                                                                                  LGRNSFEVRVCACPGRDRRTEEENFHKKGEPCPEPPPGSTKRALPPST---SSSPPQKKK
                                                                                                                                                                                                                                                                                                            VSSPPPPNTCVRAMAIYKKSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAK
                                                                                                                                                                                                                                                                                                                                    VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                                                                                                      TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                                                                                                               PLDGEYFTLQIRGRERYEMFRNLNEALELKDAQSGKEPGGSRAHSSHLKAKKGQSTSRHK
                                                                                                                                                                       SPDDELLYLPVRGRETYEMLLKIKESLELMQYLP-----
                                                                                                                                                                                                                           LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                                              PL----SSSVPSPKTYPGTYGFRLGFLHSGTAKSVTWTYSPLLNKLFCQLAKTCPVQLW 133
                                                                                                                                                                                                                                                                                                                                                                                                                ENNVLSSELCPAVDELLLPESVVNWLDE-----DSDDAPRMP--ATSAPTAPGP--APSW
                                                                                                                                                                                                                                                                                                                                                                                                                                           ENNAQTQFSEPQYTNL----GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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381 AA;
(Rel.
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                          STANDARD;
 35, Created)
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344
375
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42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 744; DB 1;
Pred. No. 6.3e-44;
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BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEES -> MQEP (IN REF. 2).
L -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
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                          PRT;
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                          386
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EMBL;
                                                  DOMAIN
DOMAIN
                                                                                                                                             PRINTS; ProDom;
                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                PIR; S51648; S51648.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dequiedt F., Kettmann R., Burny A., Willems L.; "Nucleotide sequence of the bovine P53 tumor-suppressor cDNA."; DNA Seq. 5:261-264(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellular tumor antigen p53 mp53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation updat
MOD_RES
                         MOD_RES
                                        DOMAIN
                                                                             DNA_BIND
                                                                                          DOMAIN
                                                                                                      Nuclear
                                                                                                                   Anti-oncogene; DNA-binding;
                                                                                                                                 ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                        InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES-B.indicus; STRAIN-Boran; TISSUE-Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Momori H., Ishiguro N., Horiuchi M., Shinagawa
Predominant p53 mutations in enzootic bovine 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-Bovine; STRAIN-Holstein; MEDLINE-96401400; PubMed-8807776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIES-BOVINE; TISSUE-Liver;
MEDLINE-95352829; PubMed-7626789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos indicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vet. Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 13-386 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                              OLISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis induction seems to be mediated either by stimulars and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                          X81704; CAA57348.1;
D49825; BAA08629.1;
U74486; AAB51214.1;
                                                                                                      protein;
                                                                                                                                                           PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Zebu)
385
                         94
318
361
304
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                                                                                                        Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos.
                       285
349
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385
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                                                                                                                  Transcription regulation; Activator;
                                     BASIC (REPRESSION OF NUCLEAR LOCALIZATION
PHOSPHORYLATION
                         PHOSPHORYLATION
                                                                OLIGOMERIZATION
                                                                            TRANSCRIPTION BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Thymus
                                                                                                        Apoptosis
                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
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                                                                                          ACTIVATION
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_MARMO
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036006;
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SEQUENCE
                                                                                                                                                                                                                                         MEDLINE-97376996; PubMed-9233767; Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.; Partial characterization of the woodchuck tumor suppressor, its interaction with woodchuck hepatitis virus X antigen in
                                            ++
                                                                                                                                                                                                                hepatocarcinogenesis.";
Oncogene 15:327-336(1997)
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                        Marmota monax (Woodchuck).
                                                                                                                                                                                                                                                                                                                                                                                                                 Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in of transformed cells. p53 is frequently mutate in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                            FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                       expression SUBUNIT: B:
                                                                                                  Apoptosis induction BAX and FAS antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNRRPILTITLEDSCGNLLGRNSFEVRVCACPGRDRRTEEENLRKKGQSCPEPPPRSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-LAPPOHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGG
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Rodentia;
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Pred. No. 6.5e-44;
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Sciurognathi; Sciuridae;
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RESULT 15
p53 ORYLA STANDARD; PRT; 352 AA.
ID P53 ORYLA STANDARD; PRT; 352 AA.
AC P79820; O9PSU7; Q9PSU8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor F GN TP53 OR P53.
OS Oryzias latipes (Medaka fish) (Japanese riceff OC Eukaryota; Metazoa; Chordata; Craniata; Vertek OC Actinopterygii; Neopterygii; Teleostei; Eutele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restrict the formation of the swing state of the swing state of the swing state of the swings and the swings state of the swings swings and the swings swing
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Nuclear protein; Phosphorylation;
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NUCLEAR LOCALIZATION SIGNAL (POTE
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OLIGOMERIZATION
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Vertebrata; I Euteleostei;

Euteleostomi; Neoteleostei;

suppressor p53).

update)

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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.; "Isolation of CDNAs encoding the p53 tumor suppressor gene Japanese Medaka (OTYZ1as latipes)."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Krause M.K., Rhodes L.D., van Beneden R.J.;

*Cloning of the p53 tumor suppressor gene from the Japanese medaka (Oryzias latipes) and evaluation of mutational hotspots in MNNG-exposed fish. *;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF003949; AAD01195.1; EMBL; AF003950; AAD01196.1; HSSP; P04637; IYCS.
                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANT THR-91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Himedaka;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAX and FAS antigen expression, or by repression of Bc1-2 expression (By similarity).
SUBDINIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                  117 IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN 176
                                                                                                                                                                                                      148;
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                                                                                                                                                 57 QPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP 116
                                                                                                                                                                                                                               Similarity
EPVPTNEVNPPPTTVPVTTDYPGSYELELRFQKSGTAKSVTSTYSETLNKLYCQLAKTSP
                                                                                                                                                                                                                                                                                                      352 AA;
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S -> T.
                                                                                                                                                                                                                             Pred.
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                                                                                                                                                                                                      Mismatches
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nes 67;
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                                                                                                                                      SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETR
KRKKSHSSGEEEDNREVFHFEVYGRERYEFLKKINDGLELLE 329
                                                           EGLVLGRRCFEVRICACPGRDRKTEEESRQKTQPK-----KRKVTPNT----SSS
                                                                                         DGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSI
                           KKRRS-----PDDELLYLPVRGRETYEMLLKIKESLELMQ 331
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Search completed: August 7, 2003, 09:47:27 Job time: 11.3921 secs

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Result
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Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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SP_REMBL_23:*

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Sp_bacteria

Sp_fungi:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Q9ubv9 homo sapien
Q9plb4 homo sapien
Q75080 homo sapien
Q89097 mus musculu
Q99je2 rattus norv
Q9h3d4 homo sapien
Q75195 homo sapien
Q9uel0 homo sapien
Q9uel0 homo sapien
Q9uel0 homo sapien
Q9uel0 rattus norv
Q9jjp6 rattus norv
Q9jjp6 rattus norv
Q9jjp6 rattus gall
Q9h3p8 homo sapien
Q9up26 homo sapien
Q9up26 homo sapien
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Q9up26 mus musculu
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             Q9P1B4;
Q9P1B4;
01-OCT-2000
01-OCT-2000
01-OCT-2002
P51 isoform
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                                                                                                                                                                               GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
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                                                                                          PRELIMINARY;
    (Human)
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Pred. No. 1.5
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annotation
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Best Local Sin
Matches 585;
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InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PRODOM; P000361; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
Nuclear protein.
SEQUENCE 586 AA; 65726 MW; 9
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Yokota J.
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Neoplasia 1:71-79(1999).
-i- SUBCELIULAR LOCATION: NUCLEA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AFI16758; AAF43491.1;
AFI16759; AAF43491.1;
AFI167676; AAF43491.1;
AFI16768; AAF43491.1;
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 QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
                                             DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVGFLARLGCSSCLDYFTTQGLTTIY
                                                         DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                   YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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K., Kawahara C.,
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Pred. No. 3
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Best Local Similarity
Matches 583; Conserv
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"A second p53 related protein, p73L, with high homology to Blochem. Blophys. Res. Commun. 248:603-607(1998).

-I- SUBCELULUAR LOCATION: NUCLEAR (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE P53 FAMILY.

R EMBL; ABD10155; BAA32433.1; -.

RINTETPRO; IPR001660; SAM.

R InterPro; IPR002117; P53.

R InterPro; IPR00217; P53.

R Pfam; PP00870; P53; InterPro;
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075080;
01-NOV-1998
01-NOV-1998
01-OCT-2002
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ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
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Nuclear protein.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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3 (TrEMBLrel.
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Last sequence update)
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Pred. No. 4.1e
1; Mismatches
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01-OCT-2002 (Tr
DN P63 alpha.
TRP63 OR P73H.
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                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 586 AA; 65789
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PRINTS; PR000386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
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InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Gillett E., Fleming
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                             98.8%;
98.5%;
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Last sequence update)
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                                                                                                                                                                                                                                                                             Score 3066;
Pred. No. 2.
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                                                                                                               Query Match
Best Local S
Matches 575
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Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                      -:- SUBCELLULAR LOCATION: NÚC
-:- SIMILARITY: BELONGS TO TH
EMBL; AJ277447; CAC37099.1; -
HSSP; P04637; 1YCS:
InterPro; IPR001617; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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099JE2;
01-JUN-2001
01-JUN-2001
01-OCT-2002
DN KET alpha
                                                                                                                                                                                                       SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 586 AA; 65732
                                                                                                                                                                                                                                                                                               PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1.
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Pred. No. 1
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                                                                                                                                                                                                                                                   Hagiwara F
Submitted
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Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=98448095;
                                                                                                                                                                                TISSUE-Lymph
                                                                                                                                                                                                         SEQUENCE
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K., V
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61
                                           SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQ
                                                                                                                                                                                                                                                  LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDSRRNKQQRIKEEGE
            GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                                                           SQSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAG
                                                                                                                                                     SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                                                                        SPDDELLYLPYRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSMQ
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Q9H3D4 PRELIMINARY;
Q9H3D4; Q9UP2B;
01-MAR-2001 (TIEMBLIEL 16, C:
01-MAR-2001 (TIEMBLIEL 16, L:
01-MAR-2003 (TIEMBLIEL 23, L:
TA p63 alpha (Tumor protein p
Strausberg R.;
Submitted (NOV 2002) to the submitted (NOV 2002) to the -i- SUBCELULAR LOCATION: N -i- SIMILARITY: BELONGS TO EMBL; AF124539; AAG45607.1; EMBL; AF124529; AAG45607.1; EMBL; AF124531; AAG45607.1;
                                                                                                                                                                                                                                        WEDLINE-98448000,
WEDLINE-984480000,
WENDLINE-984480000,
Wang A., Kaghad M., Wang I.,
Yang A., Kaghad M., Wang I.,
Andrews N.C., Caput D., McKeon F.;
Rof3, a p53 homolog at 3927-29, encodes multiple re-
"p63, a p53 homolog at 3927-29, and dominant-negative
"p63, a p53 homolog at 3927-29, and dominant-negative
                                                                                                                                                                                                      (JAN-1999) to
 : BELONGS TO T
; AAG45607.1;
; AAG45607.1;
; AAG45607.1;
; AAG45607.1;
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                                                                                           to the EMBL/GenBank/DDBJ dat
TION: NUCLEAR (BY SIMILARITY)
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n p63).
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   JOINED.
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EMBL/GenBank/DDBJ
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                                                                            P53
                                                                              FAMILY
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Best Local S
Matches 572
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Genew; HGNC:15979; TP63.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53; 1.
PRNOSITE; PS003681; P53; 1.
SWART; SW00454; SAM; 1.
SWART; SW00454; SAM; 1.
Nuclear Protein.
075195;
075195;
01-NOV-1998
01-NOV-1998
01-OCT-2002
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AF124533;
AF124535;
AF124536;
AF124536;
AF124537;
AF124537;
AF124537;
AF124530;
BC039815;
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                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                       TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                                                                    PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                     IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
                                                                                                   IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRETLRQ
                                                                                                                               LSMPSTSHCTPPPPPPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
                                                                                                                                                                                                                     GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                  TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                                                                                                                                                      PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                              GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                                              PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                        LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
(TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                       680 AA; 76785 MW;
                                                                                                                                                                                                                                                                                                                                                           Conservative
                              PRELIMINARY;
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AAG45607.1;
AAG45607.1;
AAG45607.1;
AAG45607.1;
AAG45607.1;
AAG45607.1;
AAG45607.1;
AAG45607.1;
AAG625635.1;
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Pred. No. 2.1e-250;
                              PRT;
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update)
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Matches 571
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Mammalia;
                                                                                                                                                                                                                                   Pfam; PF00870;
                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                      "Mutation
                                                                                                                                                                                                                                                                                                                                                                                              Yokota
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20388515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P51 isoform TAP63ALPHA
                                                                       190
              310
                                                                                                   130
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                                                                                                                                                                  Similarity
ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK
                                                                                                                                                                                                                                                                                                                                                                                                    Shimizu K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                  IPR001660; S
0870; P53; 1.
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
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-1- SUBCELLULAR LOCATION: NUC-1- SUBCELLULAR LOCATION: NUC-1- SIMILARITY: BELONGS TO THE EMBL; AB016073; BAA32593.1; -EMBL; AF116769; AAF43487.1; JC EMBL; AF116756; AAF43487.1; JC EMBL; AF116757; AAF43487.1; JC EMBL; AF116750; AAF43487.1; JC EMBL; AF116761; AAF43487.1; JC EMBL; AF116762; AAF43487.1; JC EMBL; AF116763; AAF43487.1; JC EMBL; AF116763; AAF43487.1; JC EMBL; AF116765; AAF43487.1; JC EMBL; AF116766; AAF43487.1; JC EMBL; AF116766; AAF43487.1; JC EMBL; AF116768; AAF43487.1; JC EMBL; AF116769; AAF43487; AAF448769; AAF448769; AAF448769; AAF448769; AAF448769; AAF448769; AAF448769; AAF448769; AAF448769; AAF44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 641 AA; 72019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00386; P53SUPPRESSR ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osada M., Ohba M., Kawahara C., Ishioka C., Ishawa Y., Nimura Y., Nakagawara A., Obinata "Cloning and functional analysis of human pfunctionally resembles p53.";
Nat. Med. 4:839-844(1998).
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TISSUE=Skeletal muscle;
MEDLINE=98324755; PubMed=9662378;
                                                                                                                                                                                                                                                                                                                                                                                                                              TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                            GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and expression of the 1:71-79(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002117; P53.
IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=10935472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72019 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.6%;
99.8%;
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O THE P53 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 3029;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         red. No. 4.2e
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97AE61F66E63F618 CRC64;
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p51, which
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Query Match
Best Local S
Matches 571
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Q9UE10;
01-MAY-2000
01-MAY-2000
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal muscle, and Keratinocytes;
MEDLINE-99018225; PubMed-9799841;
Augustin M., Bamberger C., Paul D., Schmale H.;
"Cloning and chromosomal mapping of the human p53-rechromosome 3q27 and its murine homolog Ket to mouse Mamm. Genome 9:899-902(1998).
                                                                                                                                                                                                                                             PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; Y16961; CAA76562.1; -.
HSSP; P04637; 1YCS;
InterPro; IPR001600; P53;
InterPro; IPR001600; SAM.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                        PROSITE; PS00348; P53; 1. Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                 Local Similarity
les 571; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
  195
                                                135
                                                                       169
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                                                                    TDYPGPHSFDVSEQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                      PYKKAEHYTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                    PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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                                                                                                                   TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
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 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                               PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSMPSTSHCTPPPPYPTDCSIVGFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 22,
                                                                                                                                                                 Conservative
                                                                                                                                                                                                              AA;
                                                                                                                                                                                                            76776 MW;
                                                                                                                                                                         97.5%;
99.8%;
                                                                                                                                                                 0,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                           Score 3025; DB 4
Pred. No. 1e-249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                           6548A6F2187D852E CRC64;
                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
                                                                                                                                                                                     4; Length
                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                     p53-related KET gene
                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                          chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                        680;
                                                                                                                                                                0;
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                       , to
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                                             194
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 254
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                                                                    Query Match
Best Local S
Matches 563
                                                                                                                                                MGD; MGI:1330810; Trp63.
Interpro; IPR002117; P53.
Interpro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  088898;
01-NOV-1998
                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                  PROSITE; PS00348; P53;
Nuclear protein.
SEQUENCE 680 AA; 767
                                                                                                                                                                                                                                                                                                                                                                                                                               TA*p63 alpha.
                                                                                                                                                                                                                                                                               transactivating, death-inducing, Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                Yang A., Kaghad M., Gillett Caput D., McKeon F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998
01-OCT-2002
                                                                                                                                                                                                                                                         -I- SUBCELLULAR LOCATION: NUCLEAR
-I- SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                                                                                                                                                                        MEDLINE=98448095;
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  ; AF075436;
; P04637; 1)
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                                                                     563;
 75
                                                                                Similarity
                                                                                                                                                                                                                                                                                                    p53 homolog at 3q27-29, encodes multiple products
                     PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
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 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSMPSTSHCTPPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
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8 (TrEMBLrel.
2 (TrEMBLrel.
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                   IYCS.
                                                                                                                                                                                                                                             AAC62641.1;
                                                                                                                                                                                                                                                                                                                                       PubMed=9774969;
                                                                                                                   76788
                                                                               96.5%;
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08,
22,
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Last annotation
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                                                                               Score 2995; DB 11;
Pred. No. 3.7e-247;
                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                          P53
                                                                                                                   8DFF0284F247C68A CRC64;
                                                                                                                                                                                                                                                                                                                           Fleming
                                                                     Mismatches
                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                     (BY SIMILARITY)
                                                                                                                                                                                                                                                          FAMILY.
                                                                                                                                                                                                                                                                                           dominant-negative
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    Query Match
Best Local Similarity
Matches 562; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99JE3;
Q99JE3;
01-JUN-2001
01-JUN-2001
01-OCT-2002
TAL KET alph
                                                                                                  PRINTS; PR00386; P53SUPPRESSR.
ProDoms; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
                                                                                                                                                                                                       HSSP; P04637; 1YCS.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: N
-1- SIMILARITY: BELONGS TO
EMBL; AJ277446; CAC37098.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                     variants.";
FEBS Lett. 501:121-126(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Wistar; TISSUE-Tongue; MEDLINE-21363378; PubMed-11470269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                    Bamberger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                'Identification and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNSMNKLPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
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      Conservative
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                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                   tissue
                                                                                      74660 MW;
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96
                       3 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17,
17,
22,
                                                                                                                                                                                                                                                                                                                 NUCLEAR (BY SIMILARITY)
THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                              distribution
  Score 2991; D
Pred. No. 7.8e
5; Mismatches
    5
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                   C953BBAC389D5B70 CRC64;
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DB 11;
1.8e-247;
nes 5;
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  Gaps
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1D Q9JJP6

1D Q9JJP6

AC Q9

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Q9JJP6;
Q1-OCT-2000
Q1-OCT-2000
Q1-OCT-2002
                                                                                                                      TISSUE-Lingual (
Schmale H.;
Submitted (APR-)
                                                                                                                                                                                                                           TISSUE-Lingual epithelium;
MEDLINE-97460723; PubMed-9315105;
Schmale H., Bamberger C.;
"A novel protein with strong homo
Oncogene 15:1363-1367(1997).
                                      -!- SUBCELLULAR LOCATION: N
-!- SIMILARITY: BELONGS TO
EMBL; Y10258; CAB88216.1; -
HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                        ros.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TA2 KET alpha.
                 InterPro;
                                                                                                                                                                                      SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNSMNKLPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
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                                                                                                                            (APR-2000)
                       IPR002117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                                                                                                      N.A.
                                                                                                                                                                 epithelium;
P53
                                                                                                                            6
                                                                               the EMBL/GenBank/DDBJ data
N: NUCLEAR (BY SIMILARITY).
TO THE P53 FAMILY.
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Last sequence up
                                                                                                                                                                                                                                                   homology
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                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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554

631

494 511 434 451

571

391

314 331 254 271

suppressor p53.

Rattus

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RESULT RESULT RESULT OF THE OFFICE ACT OF THE OFFICE ACT OF THE OFFICE ACT OF
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Best Local Similarity
Matches 562; Conserv
Yasue A.,
"Cloning and
"h. Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; pF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; pD002681; P53; 1.
SWART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
Nuclear protein.
SEQUENCE 680 AA; 76760 MW; !
                                                                                                                                                                                                                 Q9DEC7 PR
Q9DEC7;
01-MAR-2001 (T
01-MAR-2001 (T
01-OCT-2002 (T
DN p63 alpha
DNP63A.
Gallus gallus
            WEDLINE=20568966; PubMed=11118893;
Yasue A., Tao H., Nohno T., Moriyama
"Cloning and expression of a chick p6
Mech. Dev. 100:105-108(2001).
                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae;
                                                                                               SEQUENCE
                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                      12
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                                                                                            FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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1 (TrEMBLrel. 16,
2 (TrEMBLrel. 22,
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98.3%;
      a chick p63 gen
                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation updat
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Pred. No. 8.1e-247;
5; Mismatches 5;
                                                                                                                                                                           Craniata; Vertebrata; Eutel
; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                PRT;
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NCBI_TaxID=9606;

Hominidae;

EQUENCE

FROM

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-!- SIMILARLI.

EMBL; AB045224; BAb..

& HSSP; P04637; 1YCS.

& InterPro; IPR002117; P53.

DR InterPro; IPR002117; P53.

DR Pfam; PF00970; P53; 1.

DR PRINTS; PR00386; P53SUPPRESSR.

PRODOm; PD002681; P53; 1.

"""DOM; P0002681; P53; 1.
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Best Local Sin
Matches 560;
                          Delta N p73L.
Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammmalia; Eutheria; P
                                                          Q9H3P8
Q9H3P8;
Q1-MAR-2001
01-MAR-2001
01-OCT-2002
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SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53;
Nuclear protein.
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                                                                                                                                                GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                                                                                                                                                                                           YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV
                                                                                                                                       GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                                                                                         HIEHYSMDDLVSLKIPEQFRHAIWKGILDHRQLHDFSSPPHLLRTPSGASTVSVGSSETR
                                                                                                                                                                                  QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
                                                                                                                                                                                                                                           SQSSYGSNSPPLSKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGTNIPMMGTHMAMTG
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                                                          (TrEMBLrel.
                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                              PRELIMINARY;
                        Chordata;
Primates;
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95.6%;
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16,
22,
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Last sequence
Last annotation
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Pred. No. 2e-244;
                          Craniata; V
Catarrhini;
                                                                                              PRT;
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                                                           sequence update)
annotation update)
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                                   Vertebrata; Euteleostomi;
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InterPro; IPR00160; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOm; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
  Q9P1B5
Q9P1B5;
01-OCT-2000
01-OCT-2000
01-OCT-2002
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EMBL; AB04.2841; BAB20591.1; -- EMBL; AB04.2841; BAB20591.1; -- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00348; P53; 1. Nuclear protein.
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Okamoto T.,
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                                                                                                                                                                                                                   GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
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  (TrEMBLrel. (TrEMBLrel.
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Last sequence update)
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                                                                                          PRT;
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Best Local S
Matches 456
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-1- SIMILARITY: BELONGS TO THE PE
EMBL; AF116769; AAF43492.1; JOINI
EMBL; AF116759; AAF43492.1; JOINI
EMBL; AF116769; AAF43492.1; JOINI
EMBL; AF116761; AAF43492.1; JOINI
EMBL; AF116762; AAF43492.1; JOINI
EMBL; AF116763; AAF43492.1; JOINI
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EMBL; AF116765; AAF43492.1; JOINI
EMBL; AF16765; AAF4865; AA
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PRODOM; PD002681; P53; 1.
PROSTTE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 461 AA; 51305 MW:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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EMBL; AF124539; AAG45611.1; JOINED.
EMBL; AF124530; AAG45611.1; JOINED.
EMBL; AF124531; AAG45611.1; JOINED.
EMBL; AF124531; AAG45611.1; JOINED.
EMBL; AF124531; AAG45611.1; JOINED.
EMBL; AF124531; AAG45611.1; JOINED.
EMBL; AF124533; AAG45611.1; JOINED.
EMBL; AF124534; AAG45611.1; JOINED.
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Q9UP26;
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DN P63 beta.
P63.
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ProDom; PD002681; P53; 1.
PROSITE; P500348; P53; 1.
Nuclear protein.
SEQUENCE 461 AA; 51404 MW;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                             SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQQHQHLLQKQTSIQ
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Metazoa; Primates; (
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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Post-processing: Minimum Match 0%
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Wang T, Fan L; WPI; 2000-628399/60.	(CORI-) CORIXA CORP.	22-FEB-2000; 2000US-0510376.	20					03-APR-2000: 2000WO-US08896	19-OCT-2000.		WO200061612-A2.	Homo sapiens.		vaccine; detection.	Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;	and the process rockers with the second seco	Himan 163 protoin isoform #A	21-FEB-2001 (first entry)		AAB11362;		AAB11362 standard; Protein; 461 AA.	AAB11362	LT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
Chromosome aberration; oncogenic fusion protein; cancer; oncog proliferative disease; cellular protein isoform; heat shock proliferative disease; cellular protein isoform; heat shock profes; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; (
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YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV

 ${\tt LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR}$

300

VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ

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180 180 120

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61 61 Query Match Best Local S Matches 461

Similarity

100.0%;

461 AA; This is

the

amino acid

sequence of a human

oncogenic

461;

Conservative

0;

Score 2450; DB 23; Pred. No. 6.6e-195; Mismatches 0;

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60 60 0,

MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS

TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK

TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK

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oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoletic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral
                                                                                                                                                                                                                                                                                                     cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding treating genetically-defined disease with chromosomal aberration yielding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases, involves
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                          proteins (I),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-698710/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetically-defined disease associated with chromosomal ons yielding oncogenic fusion proteins, e.g. cell proliferative, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 342-344;
                                                                                                                                                                                                                                                                                                                                                                                                                        describes a method of treating genetically-defined disease th chromosomal aberrations yielding oncogenic fusion treating cancerous cells containing (I) in a heterogeneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389pp; English.
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                                                                       CC The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic CC activity, and can be used in gene therapy and in vaccines. Compositions CC comprising (I) or (II) can be used for stimulating an immune response in CC a patient and for treating lung cancer in a patient. Oligonucleotides of CC (I) can be used for detecting the presence of a cancer in a patient, by CC obtaining a biological sample from the patient, contacting the CC biological sample with the oligonucleotide, detecting in the sample, an CC amount of polynucleotide that hybridises to the CC comparing the amount of polynucleotide that hybridises to the CC comparing the amount of polynucleotide that hybridises to the CC comparing the amount of polynucleotide that hybridises to the CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to CC indicate the presence or absence of a cancer such as lung cancer.

CC ABQ92145 to ABQ92486 and ABPG1866 to ABPG1992 represent sequences used CC in the exemnification of the present towarts.
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ABQ92145
in the ex
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer
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Vedvick TS;
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RESULT 4
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Best Local Similarity
Matches 461; Conserv
                                                                                                                                                                              28-JUN-2000;
02-AUG-2000;
21-AUG-2000;
15-SEP-2000;
09-OCT-2000;
12-DEC-2000;
                                           Wang T,
McNeill
                                                                                                                                                                                                                                                                                                                                              28-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung tumour;
                     TS,
                                                                                                             CORIXA CORP
                Wang A, Skeiky YAW,
PD, Fanger N, Retter
TS, Carter D, Watan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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2000US-0630940.
2000US-0643597.
2000US-0662786.
2000US-0685696.
2000US-0735705.
2001US-0850716.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoform,
                   Y YAW, Li SX, Kalos MD, Retter MW, Marnerakis M, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461
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Pred. No. 6.6e-195;
; Mismatches 0;
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                                           Fanger
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                 Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 9 proliferative disease; cellular protein isoform; heat shock protein 9 HSP-90; rheumatoid arthrittis; cancer; haematopoiettic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                     04-DEC-2002
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Matches 460
                                                                                                                                                                                                                                                                                                                              oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell prolif diseases, involves administering an inhibitor of heat shock prot
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                                                                                                                                                                                                                                                                                               Sequence
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              CC cell regulatory proteins (CRPs) termed the p63 family of proteins, CC which demonstrate certain sequence identity to known tumour CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using CC RACE. Sequencing of the amplification product indicated that the CC amplified cDNA possessed a truncated N-terminus, i.e. the CT can be corresponded to the corresponding CC to exons 5-9 of p63. At least 6 different isotypes exist. Splice CC variants differing at the C-terminus are designated as alpha, beta CC and gamma forms, while p63 members differing in the N-terminus are CC designated as deltaN and TA forms, where the deltaN form lacks the CC transactivation domain. The present sequence represents mouse p63 corresponding CC isotype mu-deltaNp63 beta. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent CC activities, such as the ability to transactivate p53 reporter genes CC and induce apoptosis. Cessation or down-regulation of p63 expression CC may play a critical role in the process of cervical squamous of inferentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. CC catevaxia) and neuronal differentiation and related degenerative contextal and neuronal deliferentiation and related degenerative colleges (see advocated in a process of p63 act as dominant negatives towards transactivation by p53 and p63. CC catevaxia) and neuronal differentiation and related degenerative colleges (see advocated in a particle of the process of p63 colleges of p63 and p63. The process of p63 colleges of
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15-OCT-1997;
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            McKeon F,
                                                                                           02-OCT-1998;
                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                 Human cell regulatory protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX58572-83) and anti-p63 antibodies of the invention can be used identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.
                                                         29-MAY-1998;
15-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC intron-exon organisation is conserved between p/3 and p53, and from CK known exon and intron sizes for these 2 genes, it was possible to cidentify new members of this gene family using a pCR-based strategy CC identify new members of this gene family using a pCR-based strategy CC intron. The human p53 gene was localised to chromosomal position CC 3927-29. At least 6 different isotypes exist. Splice variants CC differing at the C-terminus have been designated as alpha, beta and CR designated as deltaw and TR forms, where the deltaw form lacks the CC transactivation domain. The present sequence represents human CC p63 isotype hu-deltawp63 alpha. p63 was detected in a variety CC of human and mouse tissue. It demonstrates remarkably divergent CC and induce apoptosis. Cessation or down-regulation of p63 expression CC may play a critical role in the process of cervical squamous CC act as dominant negatives towards transactivation by p53 and p63. CC act may also be implicated in haematopoiesis, muscle wasting (e.g. CC cachexia) and neuronal differentiation and related degenerative CC disorders. p63 polypeptides (see AAV58572-83) and solypeptides (see AAV58573-84), polypucleotides (see CC cathexia) and section and diagnosis, and in the production of CC cidentify compounds useful for treating disorders involving such CC cransgence animals.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-277595/23.
N-PSDB; AAX58575.
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                                       SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                                                                                         LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                   YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                                          VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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100.0%;
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Pred. No. 2.3e-192;
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MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS

Matches 456; Query Match Best Local

Similarity

98.8%; 100.0%;

Score 2421; DB 23; Pred. No. 2.3e-192; Mismatches

0;

Indels

0;

Gaps

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RESULT 8
ABG95132
ID ABG9
XX ABG9
XX ABG9
XX ABG9
XX ABG9
XX Chrc
KW Prol
KW Papi
XX Homm
XX Hom
XX H
                                                  (e.g. rheumatoid arthritis or cancer) associated with mutuant provided (e.g. recilular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papililary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell population, treating proliferative diseases associated with protein or cellular protein isoforms (II) dependent on heat shock
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        586 AA;
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                                                Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                               (CONF-) CONFORMA THERAPEUTICS
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protein (nar)-y, of structure, there is useful for chivolying administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding treating genetically-defined disease with chromosomal aberration fusion conceptic fusion protein, treating cancerous cells containing fusion conceptic fusion protein, treating calcaded with mutant protein or cellular protein in heterogeneous cell population, treating proliferative disease cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. cellular protein isoform dependent on heat shock protein or cellular protein isoform in a patient heterozygous for (II). The method is useful creating a disease e.g. haematopietic disorder such as T or B cell creating a disease e.g. haematopietic disorder such as T or B cell creating a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and carcinoma. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous protein (I), treating proliferative diseases associated with mutant cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein or cellular protein isoforms (II) dependent on heat shock protein (HSP) 90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for
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RESULT 10
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                                                                                                                                                                                                                                                                                                        Similarity
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21-FEB-2001

(first entry)

AAB11357

standard; Protein;

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Human p63 protein isoform

treatment;

human;

tumor; immunogenic; cytostatic;

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                                                                                                                                                                                                                                                                                                                                                         Sequence
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30-DEC-1999;
10-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung
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)B; AAC66027.
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SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                  SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQ
                                               SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPOHTIETYRQOQQQOHOHLLQKQTSIQ
                                                                            LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                  YVEDPITGRQSYLVPYEPPQYGTEFTTYLYNFMCNSSCYGGMNRRPILIIYTLETRDGQV 240
                                                                                                                                                                 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                              TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK. 120
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                       TFDALSPSPAIPSNTDYPGPHSSDYSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                                                                                                                                                                                                                                        586 AA;
                                                                                                                                                                                                                                                                                                            Conservative
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99US-0466396.
99US-0476496.
2000US-0480884.
2000US-0510376.
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                                                                                                                                                                                                                                                                                                                   98.1%;
99.3%;
                                                                                                                                                                                                                                                                                                    Score 2404; DB 21;
Pred. No. 6e-191;
""cmatches 2;
                                                                                                                                                                                                                                                                                                                         DB 21; Length 586;
                                                                                                                                                                                                                                                                                                     Indels
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Query Match Best Local S Matches 453

Similarity

98.1%; 99.3%;

Score 2404; DB 2 Pred. No. 6e-191; 1; Mismatches

DB 23;

Length Indels

0;

Gaps

0

60

Conservative

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The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic CC activity, and can be used in gene therapy and in vaccines. Compositions CC comprising (I) or (II) can be used for stimulating an immune response in CC (I) can be used for detecting lung cancer in a patient. Oilgonucleotides of CC (I) can be used for detecting the presence of a cancer in a patient, by biological sample with the oilgonucleotide, detecting in the sample, an CC comparing the amount of polynucleotide that hybridises to the oilgonucleotide and CC comparing the amount of polynucleotide that hybridises to the oilgonucleotide and CC comparing the amount of polynucleotide that hybridises to the configuration of a cancer in the patient. (I) and (II) are useful in CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to CC ABG92145 to ABG92868 and ABG9186 to ABG9192 represent sequences used CC in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ωy
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     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang T, Wan
McNeill PD,
                                                                                                                                                                                                                                                                                              Example 2; Page 326-328; 381pp; English.
                                                                                                                                                                                                                                                                                                                      Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-DEC-2000; 2000US-0735705
07-MAY-2001; 2001US-0850716
28-JUN-2001; 2001US-0897778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-2001; 2001WO-US47576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP61909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP61909 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang A, Skeik
PD, Fanger N,
D, Watanabe Y,
586 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky YAW, Li SX, Kalos MD, Henders
er N, Retter MW, Durham M, Fanger GR,
be Y, Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 586
                         invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TS;
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RESULT 12
ABB74989
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ID 74989
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12-DEC-2000;
07-MAY-2001;
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02-AUG-2000;
21-AUG-2000;
15-SEP-2000;
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McNeill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human p53 homologue
                                          Example 2;
                                                                             Polynucleotides encoding lung lung cancer or stimulating an
                                                                                                                                                                                                                                                                              (CORI-)
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bB; ABL49246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lung tumour;
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                                      Page 319-320; 374pp; English.
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2000US-0630940.
2000US-0643597.
2000US-0662786.
2000US-0662786.
2000US-0735705.
2000US-0735705.
                                                                                                                                                                                                 Fanger
Carter
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Watanabe Y,
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                                                                                               tumor polypeptides,
                                                                               immune
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human lung tumour proteins.
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                                                                                                                                                                                             SX, Kalos MD,
, Marnerakis M,
Y, Peckham DW;
                                                                               response
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  Human
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Lung
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Best Local Sim
Matches 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABIA4895 to ABIA4300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
             29-MAY-1998;
15-OCT-1997;
                                                                                                                                                                         Cell regulatory protein; p63; mu-deltaNp63 alpha; mouse;
                                                                                                                                                                                                   Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                 02-OCT-1998;
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                                                                                                                                                                                                                            16-AUG-1999
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             98US-0087216.
97US-0062076.
                                                 98WO-US21992
                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                 ressor; cell cycle control cell differentiation; the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.1%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2404; DB 2
Pred. No. 6e-191;
                                                                                                                                                                                                  p63, isoform
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(HARD) HARVARD COLLEGE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transactivation domain was absent. Additional splice variants were definitified by screening a cDNA library with a probe corresponding to examinate differing at the C-terminus are designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltan and TA forms, where the deltan form lacks the C transactivation domain. The present sequence represents mouse p63 classified muscle tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression cmay play a critical role in the process of cervical squamous of differentiation, both benign and neoplastic. Deltan isotopes of p63 cachexia) and neuronal differentiation and related degenerative cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAV58572-83) and pati-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. Mouse p63 cNNA was isolated using RACE. Sequencing of the amplification product indicated that the amplified cNNA possessed a truncated N-terminus, i.e. the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                              61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
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                                                                                        SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
                                                                                                                                                               LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                       YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                                                   TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                    SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSMQ
                                                                                                                                            LGRRCFEARICACPGRDRKADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                  YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                                                          VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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98.9%;
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Pred. No. 1
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1.9e-190;
hes 2;
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18-MAR-1998;
27-JUL-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer. The polypeptides and polynucleotides can be used to stimulate T cells or antigen presenting cells for use in the treatment of lung cancer. The polypeptides and monoclonal antibodies specific for the polypeptides can also be used to inhibit the development of lung cancer. Agents which bind the polypeptides can be used for detecting lung cancer and for monitoring the progression of lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated lung tumor polynucleotides, treatment, prevention and monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421
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YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                     VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                   MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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98US-0040984.
98US-0123912.
98US-0123933.
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer; therapy;
vaccine; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lung cancer-associated protein L530S.
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                                                                                                                                                                                                                                                      Wang
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                                                                                                                                                                                                                                                                                                                                                                                                             WO200061612-A2
                              This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                       WPI; 2000-628399/60.
N-PSDB; AAC65887.
                                                                                                                                                      Claim 3; Page 163-164;
                                                                                                                                                                             in a
                                                                                                                                                                                     Isolated polypeptide comprising an protein is used for detecting and m
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99US-0476496.
2000US-0480884.
2000US-0510376.
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                                                                                                                                                        261pp; English.
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                                                                                                                                                        VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
                                      SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                         SPDDELVYLPVRGRETYEMLVKIKESLELMQYLLQHTIETYRQQQQQQQHQHLLQKQTSIQ
                                                                 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
                            SPSSYGNSSPPLNKMNSMNKLPSYSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
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pred. No. 2.3e-190;
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Search completed: August Job time : 32.7931 secs 7, 2003, 09:46:27 (OTAZU) XNAJA 3DA9 ZIHT

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1 MLYLENNAQTQFSEPQYTNL......HCTPPPPYPTDCSIVRIWQV 461
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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

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; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-343
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
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Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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US-08-390-515A-8
US-08-801-718-8
US-08-047-041A-25
US-08-047-041A-26
US-08-347-792-2
US-08-390-516C-7
US-08-390-515A-6
US-08-390-515A-6
US-08-390-515A-6
US-08-390-515A-7
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pred. No. 1.2e-216;
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Mancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN CURRENT APPLICATION MUMBER: US/09/542,615A
CURRENT APPLICATION MUMBER: US/09/542,615A
MUMBER OF SEQ ID NOS: 350
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 461;
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RESULT 4
US-09-643-597-338
i Sequence 338, Application US/09643597
i Patent No. 6426072
i GENERAL INFORMATION:
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEO ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 461
TYPE: PRT
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US-09-606-421B-343
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya
APPLICANT: Hosken, Nancy
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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ACHRY, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: MCKeill, POMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C11

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 369

SOFTWARE: FastSEQ for Windown

SEQ ID NO 38

LENGTH: 586

TYPE: PPM

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US-09-42-615A-338
US-09-42-615A-338
; Sequence 338, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
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                                            APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun APPLICANT: Kalos, Michael
             APPLICANT:
                                    APPLICANT:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                      DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
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 Bangur, Chaitanya S.
Hosken, Nancy A.
Fanger, Gary R.
VENTION: COMPOUNDS AND METHODS FOR THERAPY
                                               Kalos, Michael D.
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99.3%;
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Pred. No. 2.9e-212;
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US-09-542-615A-338
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CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
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                                                                                                                                                                LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
                                                                     SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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                                                                                                                           Conservative
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99.3%;

    Mismatches

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Pred, No. 2.9e-21
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US-09-606-421B-338

US-09-606-421B-38

Sequence 338, Application US/09606421B

Sequence 338, Application US/09606421B

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Tongtong

APPLICANT: Kalos, Michael D.

APPLICANT: Hosken, Nancy

APPLICANT: Hosken, Nancy

APPLICANT: Li, Samuel X.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.
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; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-643-597-152
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US-09-643-597-152
Sequence 152, Apr
                                                  Matches 452;
                                                                Query Match
Best Local
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                                                                                                                                                  APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNEILI, Particla D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455011
CURRENT APPLICATION NUMBER: US/09/643,597
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT:
APPLICANT:
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APPLICANT:
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Li, Samuel X.
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Fan, Liqun
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Hosken, Nancy
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                                               Conservative
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99.3%;
                                                      Score 2397;
Pred. No. 1.
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Pred. No. 2.9e-212;
1. Mismatches 2;
                                         Mismatches
                                                      7; DB 4;
1.3e-211;
                                                              Length 586;
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APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
ITILE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
FILLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FALLING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTMARE: FastSEQ for Windows Version 3.0
LENGTH: 586
TYPE: PRT
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US-09-480-884A-152
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Best Local Similarity 99.1%;
Matches 452; Conservative
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                                        VMTPPPOGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAO 180
YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV 240
                          VMTPPPQGAVIRAMPYYKKAEHYTEVVKRCPNHELSREFNEGQIAPSSHLIRVEGNSHAQ
                                                                            TFDALSPSPAIDSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
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                                                                                                                                                                                    Score 2397; DB 4; Pred. No. 1.3e-211;
                                                                                                                                                                                                                Length 586;
                                                                                                                                                                                       Indels
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APPLICANT: BANGUY, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo Sapien
US-09-542-615A-152
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Best Local
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Fan, Liqun
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Pred. No. 1.3e-211;
2; Mismatches 2;
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CANCER
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-606-421B-152
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APPLICANT: Fan, I
APPLICANT: Kalos,
APPLICANT: Bangur
APPLICANT: Hosker
APPLICANT: Fanger
APPLICANT: Li, St
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                                                                 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
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Kalos, Michael D.
Bangur, Chaitanya
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Li, Samuel X.
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; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-344
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                                          GENERAL INFORMATION:
                                                      Sequence 344, Application Patent No. 6518256
    APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
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Wang, Tongto
Fan, Liqun
Kalos, Mich
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                                                                                                                                  LSMPSTSHCTPPPPPPTDCSIVRIWQV 516
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McNeill, Patricia D.
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Fan, Liqun
Kalos, Michael D.
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Fanger, Gary R.
Li, Samuel X.
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                            Tongtong.
    Michael D
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RESULT 13
US-09-606-421B-344
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                                                                                                                                                              APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitan
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
                                                                                                                                                                                                                                                                                                          Patent No. 6531315
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               Sequence 344, Application Patent No. 6531315
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LENGTH: 516
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
FILE REFERENCE: 210121.45509
CURRENT APPLICATION UMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455CB
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
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SOFTWARE: FastSEQ for
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Hosken, Nancy A.
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JREIKY, YASIT A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: MCNEILL, PATTICUS AND METHODS FOR THE THEIRTICE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C11

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 369

SEQ ID NO 339

LENGTH: 641

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; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-344
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US-09-643-597-339
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APPLICANT:
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ORGANISM: Homo sapiens -09-643-597-339
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100.0%; Pred. No. 4.8e-210;
tive 0; Mismatches 0;
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Best Local Similarity
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APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FO
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
FILE REFERENCE: 210121.455CB
FURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                      TYPE: PRT; ORGANISM: Homo sapiens US-09-542-615A-339
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SEQ ID NO 339
LENGTH: 641
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APPLICANT:
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                                                                    al Similarity 100.
442; Conservative
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100.0%; Pred. No. 3e-207;
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135 PYYKKAEHYTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194 190 PYYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194 195 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP 254 250 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP 309 255 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 314 310 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 316 315 ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQHQHLLQKQTSIQSPSSYGNGSPPLNK 374 370 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 369 111
VLV 194

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model
Scoring table:
                                    Sequence:
                                                     Title:
Perfect score:
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                                                                                                           August 7, 2003, 09:46:34; Search time 19.6814 Seconds (without alignments) 2781.719 Million cell updates/sec
                                      US-09-538-106-17
2450
1 MLYLENNAQTQFSEPQYTNL......HCTPPPPYPTDCSIVRIWQV 461
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Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters:

451899

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Published_Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 2 3 3 4 4 4 5 5 6 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
2450 2450 2450 2450 2404 2404 2397 2397 2397 2397 2379 2379 2379 2379	Score
100.0 100.0 100.0 98.1 98.1 97.8 97.8 97.8 97.8 97.1 97.1 97.1	Query Match I
461 586 586 586 586 586 516 516 541	Length DB
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US-09-735-705-343 US-09-850-716A-343 US-09-897-778-343 US-09-8735-705-338 US-09-850-716A-338 US-09-850-716A-38 US-09-735-705-152 US-09-850-716A-152 US-09-850-778-152 US-09-850-778-152 US-09-850-716A-334 US-09-850-716A-334 US-09-850-716A-339 US-09-735-705-334 US-09-850-716A-339	
Sequence 343, App Sequence 348, App Sequence 338, App Sequence 338, App Sequence 152, App Sequence 344, App Sequence 349, App Sequence 339, App Sequence 339, App Sequence 339, App	3 1 5

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sequence 36, Appl sequence 28, Appl sequence 28, Appl	Sequence 2, Appli Sequence 6, Appli Sequence 78, Appli Sequence 78, Appli Sequence 3, Appli	14049	Sequence 10, Appl Sequence 20, Appl Sequence 32, Appl Sequence 3, Appli Sequence 9, Appli	Sequence 2, Appl 1 Sequence 340, App Sequence 340, App Sequence 340, App Sequence 3, Appl 1	

ALIGNMENTS

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Query Match Best Local : Matches 46: 1	RESULT 1 US-09-735-705- US-09-735-70
	US-09-735-705-343 US-09-735-705-343 US-09-735-705-343 Sequence 343, Application of Sequence 343, Application of Sequence 343, Application of Sequence 343, Applicant of Sequence 343, Applicant of Sequence 343, Applicant of Sequence 344, A
MLYLEN MLYLEN MLYLEN	US20020052329A FORMATION Wang, Tongto Fan, Liqun Kalos, Miche Kalos, Migher Kalos, Migher Kanger, Gar Kanger, Man Kang, Aljun Kang, Aljun Kang, Aljun Kang, Migher Kanger, Mai K
tch al Similarity 100 al Similarity 100 461; Conservative 1 MIXLENNAQTQFSEP 1 MIXLENNAQTQFSEP	SULT 1 1-09-735-705-343 Patent No. US20020052329A1 Patent No. US20020052329A1 GENERAL INFORMATION: APPLICANT: AND DIAG TITLE OF INVENTION: AND DIAG TITLE OF INVENTION AND DIAG TITLE REFERENCE: CURRENT FALING DATE: CURRENT FALING DATE: CURRENT FALING DATE: CURRENT FALING DATE: CURRENT: CURRENT FALING DATE: CURRENT: CURRENT FASTSEQ for Window SEQ ID NO 343 LENGTH: 461 TYPE: PRT ORGANISM: Homo sapiens
100.0%; 100.0%; tive () FSEPQYTNI	SULT 1 :09-735-705-343 ;equence 343, Application US/09735705 gequence 343, Application US/09735705 patent No. US20020052329A1 general information: General information: General information: General information: General information: General information: Applicant: Wang, Tongtong Applicant: Hosken, Nancy Applicant: Hosken, Nancy Applicant: Wang, Aijun Applicant: Wang, Aijun Applicant: Wang, Aijun Applicant: Henderson, Robert A. Applicant: Henderson, Robert A. Applicant: Fanger, Neil ITILE OF INVENTION: COMPOSITIONS AITILE OF INVENTION: AND DIAGNOSIS TITLE OF INVENTION NOMPOSITIONS AITILE OF INVENTION NOMPOSITION NOMPOSI
; SCO ; Pre 0; M 	guence 343 Application US/09735705 guence 343 Applicant: Wang, Tongtong APPLICANT: Wang, Tongtong APPLICANT: Hosken, Nancy APPLICANT: Hosken, Nancy APPLICANT: Wang, Aljun APPLICANT: Wang, Aljun APPLICANT: McMeill, Patricia D. APPLICANT: McMeill, Patricia D. APPLICANT: McMeill, Patricia D. APPLICANT: Henderson, Robert A. APPLICANT: McMeill, Patricia D. APPLICANT: Henderson, Robert A. APPLICANT: McMeill, Patricia D. APPLICANT: McMeill, Patricia D. APPLICANT: NCMEILL, Patricia D. APPLICANT: McMeill, Patricia D. APPLICANT: COMPOSITIONS AND METRITLE OF INVENTION: AND DIAGNOSIS OF LUN TITLE OF INTENTION NUMBER: US/09/735,705 CURRENT FILING DATE: 2000-12-12 NUMBER OF SEQ ID NOS: 419 SOFTWARE: FastSEQ for Windows Version 3. SEQ ID NO 343 LENGTH: 461 TYPE: PRT ORGANISM: Homo sapiens -09-735-705-343
score 2450; pred. No. 2.: 0; mismatches (LGLLNSMDQQIQNG)	Application US/09735705 \$20020052329A1 \$20020052329A1 \$MANATION: Wang, Tongtong Fan, Liqun Kalos, Michael D. Bangur, Chaitanya S. Bangur, Chaitanya S. Hosken, Nancy Fanger, Gary R. Li, Samuel X. Wang, Aijun Skeiky, Yasir A.W. Skeiky, Yasir A.W. Skeiky, Yasir A.W. Skeiky, Yasir A.W. McNeill, Patricia D. Fanger, Neil Fanger, Neil ROMPOSITIONS AND METHONYENTION: AND DIAGNOSIS OF LUNG ENCE: 210121.455C14 ENCE: 210121.455C14 ENCE: 2000-12-12 SEQ ID NOS: 419 FastSEQ for Windows Version 3.0 43 61 Homo sapiens -343
h 100.0%; score 2450; DB 9; Length 401; Similarity 100.0%; pred. No. 2.5e-197; Indels 0; Gaps 61; Conservative 0; Mismatches 0; Indels 0; Gaps 1; Conservative 0; Mismatches 0; Indels 0; Gaps 1; MIXLENNAQTQESEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 1; MIXLENNADQQIQNGSSTSPYNTDHAQNSVTAPSPYAQPSS 1; MIXLENNADQQIQNGSSTAPSPYAQPSS 1; MIXLENNADQQIQNGSSTAPSPYNTDHAQNSVTAPSPYAQPS 1; MIXLENNADQQIQNGSSTAPSPYNTDHAQNSVTAPSPYAQPS 1; MIXLENNADQQIQNGSSTAPSPYNTDHAQNSVTAPSPYAQPS 1; MIXLENNADQQIQNGSSTAPSPYNTDHAQNSVTAPSPYAQPS 1; MIXLENNADQQIQNGSSTAPSPYNTDHAQNSVTAPSPYAQPS 1; MIXLENNADQQIQNGSSTAPSPYNTDHAQQQIQNGS 1; MIXLENNADQQIQNGSSTAPSPYNTDHAQQQIQNGS 1; MIXLENNADQQIQNGSSTAPSPYNTDHAQQQIQNGS 1; MIXLENNADQQIQNGS 1; MI	ton US/09735705 29A1 29A1 gtong chael D. chattanya S. aary R. 1 X. un asir A.W. Robert A. Patricia D. Petricia D. Patricia D.
9; Lo 197; 0; Ii rspynt 	T H
Length 401; Indels C TINDHAQNSVTAE	THERAPY
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APPLICANT: Kalos, Michael D.

APPLICANT: Malos, Michael D.

APPLICANT: McNeill, Patricia D.

APPLICANT: McNeill, Patricia D.

APPLICANT: MCNeill, Patricia D.

APPLICANT: MCNEILL, PATRICIA SAND METHODS FOR THE TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C15

CURRENT APPLICATION NUMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 440

SOFTWARE: FASTSEQ FOR Windows Version 3.0

LENGTH: 461

TYPE: PRT

ORGANISM: Homo Sapiens

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                                     181 YVEDPITGRÓSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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APPLICANT: "datanabe, Yoshihiro
APPLICANT: Henderson, Robert A.

APPLICANT: Peckham, David W.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

CURRENT APPLICATION NUMBER: US/09/897,778

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 467

SEQ ID NO 343

LENGTH: 461

TYPE: PRT

TYPE: PRT
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Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Weil
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US-09-897-778-343
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Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 338

LENGTH: 586

TYPE: PRT

ORGANISM: Homo sapien®

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Matches 453;
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RESULT

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APPLICANT: Wang, Ton
APPLICANT MATNERAK
APPLICANT Fanger,
APPLICANT Vedvick,
APPLICANT Carter,
APPLICANT Watanabe
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CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
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APPLICANT: Kalos, Michael D.
APPLICANT: MCNeill, Patricia
APPLICANT: Retter, Marc W.
                                                                                                                                                                         Sequence 338, Application US/09897778 Patent No. US20020147143A1
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 TITLE
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                INVENTION:
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Similarity 99.3%;
                                       Carter, Darrick
Watanabe, Yoshihiro
Henderson, Robert A.
Peckham, David W.
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                                                                                                  Fanger, Gary R. Vedvick, Thomas S.
                                                                                                                                Marnerakis, Margarita
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COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
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Pred. No. 2.6e
1; Mismatches
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2.6e-193;
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; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,77
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PastSEQ for Windows Version 4.
; SEQ ID NO 338
; LENGTH: 586
; LYPE: PRT
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Patent No. US
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Best Local Similarity
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 152
                                       CURRENT APPLICATION NUMBER: US/09/735,705 CURRENT FILING DATE: 2000-12-12
                                                            APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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Pred. No. 2.6e-193;
1; Mismatches 2;
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; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows VG
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-850-716A-152
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: Sequence 152, Application US/09850716A

: Patent No. US20020115139A1
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Best Local Similarity
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-09-735-705-152
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APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE REFERENCE: 210121.455C15
                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/850,716A CURRENT FILING DATE: 2001-05-07
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                                                                                                                 Similarity
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                                         MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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Pred. No. 1e-192;
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APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-152
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US-09-897-778-152
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APPLICANT: Wang, Tone
APPLICANT: Warnerak'
APPLICANT: Fanger,
APPLICANT: Vedvick,
APPLICANT: Carter, I
APPLICANT: Watanabe,
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Best Local Similarity
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                                                                                            TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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Watanabe, Yoshihiro
Henderson, Robert A.
Peckham, David W.
YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV 240
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Pred. No. 1e-192;
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US-09-466-396A-152
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Matches 452
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CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
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             DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                                                       SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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                                                           SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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o. US20030119763A1
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99.1%;
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Pred. No. 1e-192;
2; Mismatches 2;
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RESULT 12
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-344
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            Sequence 344, Application US/09850716A Patent No. US20020115139A1
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GENERAL
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LENGTH: 516
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CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
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SOFTWARE: FastSEQ for Windows Version
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nes 447; Conservative
INFORMATION:
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Fan, Liqun
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Hosken, Nancy
Fanger, Gary R.
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Pred. No. 2.7e-191;
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APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricla D.
APPLICANT: McNeill, Patricla D.
APPLICANT: McNeill, Patricla D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION UNMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
APPLICANT: Watanabe, Yoshibiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Panger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-344
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US-09-897-778-344
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APPLICANT: Marner
APPLICANT: Fanger
APPLICANT: Vedvic
APPLICANT: Carter
APPLICANT: Watana
APPLICANT: Hender
APPLICANT: Peckha
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Vedvick, Thomas S.
Carter, Darrick
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ilarity 100.0%;
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Pred. No. 2.7e-191;
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; SOFTWARE: FastSEQ for Wil

; SEQ ID NO 344

; LENGTH: 516

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-897-778-344
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                  APPLICANT: Franger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT EPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
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Best Local :
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ORGANISM: Homo sapiens -09-735-705-339
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McNeill, Patricia D.
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Bangur, Chaitanya
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Sequence 339, Application US/09850716A

Patent No. US20020115139A1

GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOUTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
CREANISM: USCO SERVICES
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US-09-850-716A-339
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Search Job ti	Qу	Qy Db	Оy	QУ	Qу	Db
Search completed: August 7, 2003, 09:57:11 Job time : 21.6814 secs	QY 435 LSMPSTSHCTPPPPYPTDCSIV 456	QY 375 MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP	QY 315 ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK 	QY 255 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 	QY 195 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP 	Db 190 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
		PP 434 PP 489	NK 374 	GR 314 	CP 254 CP 309	LV 249

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JH0031 Cellular tumor antigen p53 - rainbow trout C;Species: Oncorhynchus mykiss (rainbow trout) C;Species: Oncorhynchus mykiss (rainbow) C;Accession: J40631; A;Title: Rainbow trout p53: CDNA cloning and biochemical characterization. A;Reference number: J40631; MUID:92210006; PMID:1339362 A;Reference number: J40631; MUID:92210006; PMID:1339362 A;Residues: 1-396 (CDEF) A;Residues: 1-396 (CDEF) A;Experimental source: liver C;Superfamily: cellular tumor antigen p53 C;Superfamily: phosphoryl-RNA (Ser) DNA binding; homotetramer; nucleus; p;164,167,227,231/Binding site: phosphoryl-RNA (Ser) Covalent) #status predicted C;Superfamily: cellular control; DNA binding; homotetramer; nucleus; p;164,167,227,231/Binding site: phosphoryl-RNA (Ser) Covalent) #status predicted	30 123 5.0 969 2 T15446 31 123 5.0 947 2 T23107 32 121.5 5.0 947 2 T23107 33 120.5 4.9 901 2 JC6093 34 120 4.9 864 2 T04518 36 119 4.9 1145 2 T18235 37 119 4.9 1145 2 T32008 38 118.5 4.8 513 2 T41011 39 118.5 4.8 1062 2 G86325 40 118 4.8 1062 2 T26050 41 118 4.8 792 2 T26050 42 117.5 4.8 596 2 S39580 43 117 4.8 596 2 S39580 44 117 4.8 596 2 T303908 43 117 4.8 596 2 T303908 44 117 4.8 596 2 T228888 45 116.5 4.8 578 2 T228888
p-1999 #text_change 10-Sep-1999 ; Baney, C.; May, P.; Soussi, T. l biochemical characterization. MID:1339362 PIDN:AAA49605.1; PID:g213829 tumor suppressor gene, p53, whose inactiv tumor suppressor gene; psi, whose inactiv cys, Cys, Cys) #status predicted valent) #status predicted valent) #status predicted	hypothetical prote SNF2alpha protein hypothetical prote dead ringer nuclea hypothetical prote transcription acti hypothetical prote transcription acti hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote developmental cont developmental cont eyelid - fruit fly hypothetical prote

RESULT 2 A29376	рь	Qy	DЪ	Qy	Db	Qy	Db	Qy .	Ф	Qy	Db .	Qy	Matches	Query N
	360 DXYRQX 365	339 ETYRQQ 344	300 MKEASLPAPQPGASKKTKSSPAVSDDEIYTLQIRGKEKYEMLKKFNDSLELSELVPVADA 359	284 FRQ-NTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 338	240 ILTITLETQEGQLLGRRSFEVRVCACPGRDRKTEEINLKKQQETTLETKTKPAQGIKRA 299	227 ILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRP 283	180 RGHLVRVEGNORSEYMEDGNTLRHSVLVPYEPPOVGSECTTVLYNFMCNSSCMGGMNRRP 239	167 PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNEMCNSSCVGGMNRRP 226	121 LFCQLAKTCPVQIVVDHPPPPGAVVRALAIYKKLSDVADVVRRCPHHQSTSENNEGP-AP 17	107 LYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAP 166	61 VSATEPAPQPSISTLDTGSPPTSTVPTTSDYPGALGFQLRELQSSTAKSVTCTYSPDLNK 120	49 VTAPSPYAQPS-STEDALS-PSPAIPSNTDYPGPHSEDVSEQQSSTAKSATWTYSTELKK 106	169; Conservative 47; Mismatches 79; Indels 11; Gaps	Query Match 34.3%; Score 839.5; DB 1; Length 396; Rest Local Similarity 55.2%; pred No 9.4e-53;
			9	8	9	w	9	6	9	6	0	6	0	

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cellular tumor antigen p53 - African clawed frog C;Speciles: Kenopus laevis (African clawed frog) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A29376; S61531; S72313; I51639 R;Soussi, T.; de Fromentel, C.C.; Mechali, M.; May, P.; Kress, M.
                                                                                                                              N;Alternate names: nuclear oncoprotein C;Species: Gallus gallus (chicken) C;Date: 10-Sep-1999 #sequence_revision C;Accession: S02193
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A;Title: Cloning and characterization of a cDNA from Xer A;Reference number: A29376; MUID:88143684; PMID:2830576
     A;Residues: 1-367
                                          A; Accession:
                                                        A; Title: Nucleotide sequence of a cDNA encoding the chicken A; Reference number: S02193; MUID:89083584; PMID:3060861
                                                                                         R;Soussi, T.; Begue, A.; Kress, M.; Stehelin, Nucleic Acids Res. 16, 11383, 1988
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A;Molecule type: mRNA
A;Residues: 1-51,'S',53-70,72-293,295-363 <HOW>
A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1;
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A; Residues: 1-293,295-363 <HOE>
A; Cross-references: EMBL: X77546; NID: 9468513; PIDN: CAA54672.1; PID: 9468514
R; Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, W.
submitted to the EMBL Data Library, March 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; R;HOever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-363 <SOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A29376
                   Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: cellular tumor antigen p53
Keywords: apoptosis; cell division control; DNA binding; homotetramer; nu. 150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362/Binding site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYMEDVNS
                                                                                                                                                                                                                                                                                                                                          PDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT
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                                                                                                                                                 10-Sep-1999 #text_change
                                                                                                                                                                                        p53
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                                                                                                            D.; May, P.
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-386 <DEGO
A;Cross-references: EMBL:x81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
A;Cross-references: EMBL:x81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
C;Superfamily; cellular tumor antigen p53
C;Superfamily; cellular tumor antigen p53
C;Reywords: apoptoois; cell division control; DNA binding; homotetramer; phc
E;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) *status predicted
F;385/Binding site: phosphoryl-RNA (Ser) (covalent) *status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R. submitted to the EMBL Data Library, September 1994 A;Description: Nucleotide sequence of the ovine p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellular tumor antigen p53 - bovine N;Alternate names: tumor-suppressor protein C;Species: Bos primigenius taurus (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-
C;Accession: S51648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 41.5
54; Conservative
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                                                                                                                                                                                                                                            EPSAPAAPPPAT ----PAPATSWPLSSFVPSQKTYPGNYGFRLGFLQSGTAKSVTCTYS
                                                                                                                                                                                                                                                                                                         ---SPYAQPSSTFDALSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYS 101
G-LAPPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGG
                                                      GQTAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGG
                                                                                                                                                                            TELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 744; DB 1;
Pred. No. 6.5e-46;
5; Mismatches 120;
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A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2 (Superfamily: cellular tumor antigen p53 (C; Keywords: apoptosis; cell division control; DNA binding; homotetramer; F;174.177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predict F;390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
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A;Note: the nucleotide sequence was submitted to the C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA314 R;Hulla, J.E.; Schneider, R.P. Nucleic Acids Res. 21, 713-717, 1993 A;Title: Structure of the rat p53 tumor suppressor gene. A;Reference number: S41149; MUID:93181268; PMID:8441680
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A; Residues: 1-173, 'W', 175-391 <HUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein A; Reference number: S02192; MUID:89083585; PMID:3060862 A; Accession: S02192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Soussi, T.; de Fromentel, C.C.; Breugnot, C.;
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Best Local S
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                                                                                                                                                                                                                                                                         153 TRVRAMAIYKKSQHMTEVVRRCPHHE---RCSDGDGLAPPQHLIRVEGNPYAEYLDDRQT
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                                         FTLKIRGRERFEMFRELNEALELK----
                                                                           LYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYG
                                                                                                                   VRVCACPGRDRRTEEENFRKKEEHCPELPPGSAKRALPTST----SSSPQQKKKPLDGEY
                                                                                                                                                     ARICACPGRORKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDEL
                                                                                                                                                                                             FRHSVVVPYEPPEVGSDYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFE
                                                                                                                                                                                                                                                                                                             AVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEGNSHAQYVEDPIT
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                                                                                                                                                                                                                                                                                                                                                                                                                              TATGSPNSMEDLFLPQDVAELLEGPEEALQVSAPAAQEPGTEAPAPVAPASATPWPLSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNLGLLNSMDQ------QIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.5%; Score 723; DB 1;
41.1%; Pred. No. 2.1e-44;
tive 64; Mismatches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:CAA31457.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 391;
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                                     A; Molecule type: DNA
A; Residues: 1-393 <LAM>
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A;Cross-references: EMBL:X01405; R;Buchman, V.L.; Chumakov, P.M.;
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A;Title: Tire Com. 17. A;Reference number: JH0633; MUID:9221000/; Fi A;Accession: JH0633 A;Accession: JH0633 A;Accession: JH0633 A;Accession: JH0633 A;Accession: JH0633 A;Accession: JH0633; MUID:9221000/; Fi A;Acc
                                    MOI. Cell. Biol. 6, 1379-1385, 1986
A;Title: Characterization of the human p53
A:Reference number: A25224; MUID:87064416;
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C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nuc;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nuc;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nuc;Keywords: apoptosis; cellular zinc (Cys. His, Cys. Cys.) #status predicted F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-19
A; Reference number: A25224;
A; Accession: A25224
                                                                                                                                                                                  R; Lamb,
                                                                                                                                                                                                              C;Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000 C;Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397; 4905; I58354; I78850; I52681; S60153
                                                                                                                                                                                                                                                                                                                                                       C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                cellular tumor antigen p53 [validated] - human N_{\ell}Alternate names: cellular phosphoprotein p53
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A; Title: The cDNA cloning
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PMID: 2946935
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GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

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A; Nolecule type: mRNA
A; Nolecule type: mRNA
A; Residues: 1-71, 'P', 73-78, 'T', 80-393 <HAR2>
A; Residues: 1-71, 'P', 73-78, 'T', 80-393 <HAR2>
A; Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell lin
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell lin
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell lin
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell lin
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A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell lin
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell lin
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell lin
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell lin
A; Experimental source: clone p53-H-19, transformed h
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A;Residues: 1-71,/p',73-393 <ZAK>
A;Reference: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210
R;Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
A;Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular A;Reference number: A55060; MUID:85267676; PMID:3894933
A;Accession: A55060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Mol. Cell. Biol. 6, 4650-4656, 1986
A; Title: Molecular basis for heterogeneity of the human p53 protein.
A; Reference number: A93086; MUID:87089826; PMID:3025664
A; Accession: A25397
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A; Residues: 1-71,'p',73-393 <BUC2>
A; Residues: 1-71,'p',73-393 <BUC2>
A; Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476
A; Note: this 72-Pro allele was found in both normal and malignant cell line
R; Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
submitted to the EMBL Data Library, August 1990
                                                    A; Experimental source:
                                                                                                                                                                                                                                                     A; Molecule type: mRNA; DNA
A; Residues: 66-71, 'p',73-79 <MKI2>
A; Experimental source: clone lambda Cll3
A; Note: 72-Cys was also found, and appear
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Primary structure polymorphism at amino acid residue A; Reference number: S42452; MUID:87144273; PMID:3547088 A; Accession: S42452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Mol. Cell. Biol. 7, 961-963, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-78,'T',80-393 <HAR1>
A;Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A;Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
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A;Molecule type: mRNA
A;Residues: 1-71, 'p',73-272, 'H',274-393 <HAR>
A;Cross-references: GB:K03199; NID:g189478; PIDN:AAA59989.1; PID:g189479
A;Experimental source: clone pR4-2, cell line A431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; R;Matlashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, EMBO J. 3, 3257-3262, 1984
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A; Accession: S40773
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A; Residues: 1-393 <BUC1>
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A; Residues: 1-393 <CHU>
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A;Note: this 72-Arg allele appears to be about 5 times more
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A; Residues: 101-393 < MKI1>
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                                                                                                   66-79 <MKI3>
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F.;
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Vousden,
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     K.H.;
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     Crook,
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L.; Benchimol,
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A;Molecule type: mRNA
A;Residues: 1-247,'Q',249-393 <F08>
A;Cross-references: EMBL:X60017; NID:g506446;
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A; Residues: 1-247, 'Q', 249-393 <F06>
A; Cross-references: EMBL: X60015; NID: g506442;
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A;Residues: 1-192,'R',194-393 <F02>
A;Cross-references: EMBL:X60011; NID:g506434;
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A; Residues: 1-189, 'LLSIAEWKEICVWSIWMTETLEDIVWWCPMSRLRLALT', 'VPPSTTTTCVTVPAWAA'
A; Cross-references: EMBL.X60010; NID:g506432; PIDM:CAA42625.1; PID:g506433
A; Note: deletion of a C nucleotide causes a frameshift at position 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 10, 2879-2887, 1991
A; Title: p53 is frequently mutated in Burkitt's lymphoma cell lines
A; Reference number: I38082; MUID:92007731; PMID:1915267
                                                      Cancer Res.
                                                                                                                                                                                                                                                                                                                   A; Note: all sequences submitted to the R; Futreal, P.A.; Barrett, J.C.; Wisemar Nucleic Acids Res. 19, 6977, 1991
                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453 A;Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 19 R;Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-253, 'D', 255-393 <F11>
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A; Residues: 1-71,'P',73-162,'H',164-393 <F09>
A; Cross-references: EMBL:X60018; NID:g506448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A; Cross-references: EMBL: X60016; NID: g506444;
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                                                      A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; R;Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, JCancer Res. 51, 5800-5805, 1991
                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-393 <FUT>
                                                                                                                                                                                                           A;Status: translated from
                                                                                                                                                                                                                                    A; Accession: I38093
                                                                                                                                                                                                                                                            A; Title: An Alu polymorphism intragenic to the TP53 gene
A; Reference number: I38093; MUID:92107726; PMID:1762941
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A; Residues: 1-212,'Q',214-393 <F10>
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A; Residues: 1-236, 'I', 238-393 <F05>
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A; Residues: 1-245, 'T', 247-393 <F04>
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A; Residues: 1-393 <F03>
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                           p53
gene mutations
number: A44905;
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in gastric cancer metastases MUID:92034678; PMID:1933850
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J.; Hirohashi,
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RESULT
S06594
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A;ResIdues: 3-44 <PET>
A;ResIdues: 3-44 <PET>
B;Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
A;Title: Nuclear and nucleolar targeting sequences of c-erb-A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Molecule type: mRNA
A:Roslotus: 327-331, 'DQTSFQKENC' <CHO>
A:Residues: 327-331, 'DQTSFQKENC' <CHO>
A:Residues: 327-331, 'DQTSFQKENC' <CHO>
A:Ross-references: GB:S66666; NID:9436292; PIDN:AAB28601.1; PID:9436293
A:Note: mutant sequence with altered splicing and termination expressed in Mo
R:Petersen, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1995
A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with
A:Reference number: S60151; MUID:96133682; PMID:8552047
A:Accession: S60153
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A; Residues: 274-277, /S', 279-282 <HEN2>
A; Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1;
R; Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
A; Title: Alternative splicing of the p53 tumor suppressor gene A; Reference number: 152681; MUID:94036762; PMID:8221626
A; Accession: 152681
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antigen
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Pred. No. 2.8e-43;
0; Mismatches 98
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Nucleic Acids Res. 17, 8375, 1989

Nucleic Acids Res. 17, 8375, 1989

A;Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosp A;Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosp A;Reference number: S06594

A;Accession: S06594

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Residues: 1-393 <ARIGS

A;Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796

A;Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796

C;Superfamily: cellular tumor antigen p53

A; C;Superfamily: cellular tumor antigen p
A; Notecular type: mRNA
A; Molecule type: mRNA
A; Residues: 1-159, 'H', 161-167, 'G', 169-233, 'I', 235-390
A; Cross-references: GB:X01237; GB:K01700; NID:953575
A; Cross-N-Nomitra, D.; Yokota, K.; Wolf, D.; Brill, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 306, 594-597, 1983
A; Title: A single gene and a pseudogene for A; Reference number: A02684; MUID: 84068204; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Primary structure of DNA complementary to murine A;Reference number: S06336; MUID:88221682; PMID:3329909 A;Accession: S06336
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A;Title: Analysis of the gene coding for the murine cellular A;Reference number: A22739; MUID:85027173; PMID:6092064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: oncoprotein p53
C;Specias: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C;Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S06594
R;Rigaudy, P.; Eckhart, W.
                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-134, 'V', 136-390 <CHU>
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                                                                                                                                                                           A; Accession: A02684
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48.9%;
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Pred. No. 5.8e-43;
                                                                                                                                                                                                                                                                                                                                   B.; Lavie, V.; Hazum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                   c the cellular PMID:6646235
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E.; Shohat,

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F;313-319/Region: nuclear location signal
F;319-357/Region: tetramer association
F;79,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F;389/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted
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A; Residues: 1-47, R, 49-78, OW', 82-390 < RES>
A; Residues: 1-47, R, 49-78, OW', 82-390 < RES>
A; Cross-references: EMBL:X00741; NID:953570; PIDN:CAA25323.1; PID:953571
C; Comment: This DNA-binding protein plays an essential role in the regula
C; Comment: The tetramer association region may exhibit a beta-turn, beta-
C; Commently: cellular tumor antigen p53
C; Keywords: apoptosis; cell division control; DNA binding; homotetramer;
E; 1-44/Domain: transcription activation #status predicted <TRA>
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F;114-139/Region: conserved region
F;160-192/Region: L2 loop
F;168-178/Region: conserved region
F;231-252/Region: conserved region
F;233-248/Region: L3 loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross references: EMBL:M13873
R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; submitted to the EMBL Data Library, July 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Cell. Biol. 6, 3434-3439, 1900
A;Title: Immunologically distinct p53 molecules generated by alternative splicing.
A;Reference number: S38822; MUID:87064640; PMID:3023970
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A; Residues: 1-167, 'G',169-233, 'I', 235-390
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F;99-289/Domain: DNA-binding core #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1; R;Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A. Nucleic Acids Res. 12, 5609-5626, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-167, 'G', 169-390 < ARA3>
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A; Accession: S40014
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                                                                                         KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
                                                                                                                                                                                NSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDST
                                                                                                                                                                                                                                                          SREFNEGO-IAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLXNFMC
                                                                                                                                                                                                                                                                                                                                     VMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHE-
                                                                                                                                                                                                                                                                                                                                                                ATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHEL 155
                                               LPPGSAKRALPTCT---SASPPQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---
                                                                                                                                        NSSCMGGMNRRPILTITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEVLCPE
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43.2%; Pred. No. 6.8e-43;
tive 54; Mismatches 97;
TYROQQQQQHQHLLQKQTSIQS
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R;Lee, H.; Larner, J.M.; Hamlin, J.L. Gene 184, 177-183, 1997
A;Title: Cloning and characterization of Chinese hamster A;Reference number: JC6176; MUID:97183659; PMID:9031625
A;Contents: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: p53
C;Superfamily: cellular
C;Keywords: tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rile Goas, F.; May, P.; Ronco, P.; de Fromentel, C.C. dene 185, 169-173, 1997

A:Title: cDNA clonding and immunological characterization A:Reference number: JC6193; MUID:97208869; PMID:9055811

A:Accession: JC6193...
C;Superfamily:
C;Keywords: liv
                                                                                                     A;Cross-references: GB:U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230 C;Comment: This protein is a multimer, it plays the central role in a comp
                                                                                                                                                                                                                                                                                                                                           tumor suppressor protein p53 - Chinese C; Species: Cricetulus griseus (Chinese C; Date: 11-Apr-1997 #sequence_revision
                                          A;Gene: p53
                                                               C; Genetics:
                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-393 <LEE>
                                                                                                                                                                                      A; Accession: JC6176
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A; Residues: 1-391 <LEA>
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
                                                                                     iption,
                                                                                                                                                                                                                                                                                                                           C; Accession: JC6176
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Pred. No. 9.
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hamster)
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F;108-121/Region: L1 loop
F;114-139/Region: conserved region II
F;160-192/Region: conserved region II
F;168-178/Region: conserved region III
F;231-252/Region: conserved region IV
F;233-248/Region: conserved region V
F;267-283/Region: conserved region V
F;313-319/Region: nuclear location sign
F;313-319/Region: tetramer association
F;7,9,12,18,23,37/Binding site: phosphafe
F;173,176,335,239/Binding site: zinc (C
F;312/Binding site: phosphate (Ser) (co
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A;Title: Immunologically distinct p53 molecules generated by alternative spl A;Reference number: S38822; MUID:87064640; PMID:3023970
A;Accession: S38824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cellular tumor antigen p53, minor splice form - mouse C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C;Accession: S38824; S35478
                                                                                                                                                                                                                                                                           C;Superfamily: cellular tumor antigen p53
C;Keywords: alternative splicing; phosphoprotein;
F;1-44/Domain: transcription activation *status p;
                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988 C;Comment: This sequence, produced by alternative splicing of the tenth intron, li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Han, K.A.; Kulesz-Martin, M.F.
Nucleic Acids Res. 20, 1979-1981, 1992
A;Title: Alternatively spliced p53 RNA in transformed and A;Reference number: S35478; MUID:92253421; PMID:1579500
A;Accession: S35478
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A; Residues: 1-381 <HAN>
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A; Residues: 1-381 < ARA>
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Best Local S
Matches 143
313-319/Region: nuclear location signal
319-357/Region: tetramer association
319-357/Region: tetramer association
7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
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;99-289/Domain: DNA-binding core
                                                                                                                                                                                                                                                                                                                                         not known
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47.2%; Pred
47.2%; 52;
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Pred. No. 1.4e-42;
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                                                                                                                                                           RESULT 14
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                                                            R; White, S.
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A; Gene: p53
A; Introns: 24/1
C; Superfamily:
submitted to the EMBL Data A; Reference number: Z19114 A; Accession: T19361
                                                                         hypothetical protein C17G1.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T19361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L27630;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The canine p53 gene is subject to somatic mutations A;Reference number: 140226; MUID:95150524; PMID:7847847 A;Accession: 146226 A;Cession: 146226 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellular tumor antigen p53 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
C;Accession: I46226
R;Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Continuous Res. 14, 2039-2046, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-77 < DEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 144; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                              139 KAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEP 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 AQNSVT-APSPYAQPSSTFDALSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKS
                                                                                                                                                                                                                                                                                                          μ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POVGTEFTTVLYNFMCNS
                                                                                                                                                                                                                                                                                                          KSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAKYLDDRYTFRHSVVVPYEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AHATEESGDSRAHSSLQPRAFQALIKEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQDPVTETPGPVA-----PAPATPWPLSSFVPSQKTYQGNYGFHLGFLQSGTAKS
                                                                                                                                                                                                                              PEVGFDYTTIHYNYMCNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPPGSAKRALPTCT---SASPPQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMCTYSPPLNKLFFQLAKTCPVQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellular tumor antigen p53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                     10.6%; Score 259.5; DB 2 60.3%; Pred. No. 4.2e-12;
                                     Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID:g508454; PIDN:AAC37327.1;
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Pred. No. 6.1e-42;
6; Mismatches 94
                                     August 1996
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protein-tyrosine kinase (EC 2.7.1.112) abl -
C;Species: Drosophila melanogaster
C;Date: 15-Nov-1984 #sequence_revision 30-Sep
C;Accession: A28128; A00628
                                                           A; Title: Nucleotide sequences of the Drosophila src and A; Reference number: A00628; MUID:84082064; PMID:6317185
                                                                                              A;Cross-references: GB:M19692; GB:M18402; NID:g158598; PIDN:AAA28934.1; R;HOffmann, F.M.; Fresco, L.D.; Hoffman-Falk, H.; Shilo, B.Z. Cell 35, 393-401, 1983
                                                                                                                                                                                                                                                R;Henkemeyer, M.J.; Bennett, R.L.; Gertler, F.B.; Mol. Cell. Biol. 8, 843-853, 1988
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A; Introns: 40/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-925 <WIL>
     A; Residues:
                                             A; Accession:
                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1520 <HEN>
                                                                                                                                                                                           A; Reference number: A28128; A; Accession: A28128
                                                                                                                                                                                                             A; Title: DNA sequence, structure, and tyrosine kinase activity A; Reference number: A28128; MUID:88174728; PMID:2832740
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Best Local Similarity
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                       Molecule
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type: DNA
: 'A',375,'AQ',378-644,'VGDV'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 YLENN-----AQTQF-SEPQYTNLGLLN----SMDQQIQNGSSST------
                                           A00628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAKSATWTYSTELKKLYCQIAKTCPIQIK----VMTPP----PQGAVIR-----AMPVYK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTLHVGPNDKVHPQVEKHYFSRKRQQLRVPYP-----EGINSHTTPPTEPNTFGFMQGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAEHV---TEVVKRCPNHELSREFNEGQIAPPSHLIRVEG-NSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVPIRHSPSQMPTHLQSPVHPSPNGAPPA-YNAPSSSKT-PDPTQQQRPHS--PTFAVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                              ANHMGGMQPMNGTPTEGPTVNNIGLNSNNAAGLPPLSLRSQGPDGSQNNDFPGIPSTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGDMNGLSPTQALP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGGSQLPSLSAPSLQRADSMPQLPSQQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPSSRGSMDQRQLQQQQIQMQQY-HQH----MQMQKMQQQQMAAQQQMSRMGGSGPSSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSI----QSPSSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; 98/2; 295/1;
collagen alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL:278415; PIDN:CAB01670.1; GSPDB:GN00028; CESP:C17G1.4 se: clone C17G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SQSMHTPMISPNFNAS------QPSTSGRQ--PAKKARSASDASEPPFNVPH 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPM 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.6%;
23.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 138; DB 2; Length 925; Pred. No. 0.067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                            30-Sep-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                                                                                      Hoffmann,
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                                                                           abl homologs:
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                                                                                                                                                                                                                                   melano
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A;Cross-references: FlyBase:FBgn0000017
A;Introns: 112/1; 130/1; 310/2; 449/1; 644/3; 735/1; 77
C;Superfamily: Drosophila protein-tyrosine kinase abl;
C;Keywords: ATP; autophosphorylation; phosphoprotein; pr: 211-260/Domain: SH3 homology <SH3>
F;211-260/Domain: SH3 homology <SH2>
F;371-363/Domain: Brotein kinase homology <KIN>
F;394-402/Region: protein kinase ATP-binding motif
F;417/Active site: Lys #status predicted
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                                                                            NAAASLNKLQRHRTTTEGTMMTFSSFRAGGSSSSPKRSASGVQPALANLEFPPPPL 1077
                                                                                                                    GMGANIPMM-----GTHMPM-----
                                                                                                                                                                                                 QQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQ----RNALTPTTIPD
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DLPPPPEEFEGGPPPPPPAPESAVQAIQ 1105
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                                     SM---PSTSHCTPPPPYPTDCSIVRIWQ 460
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Search completed: August 7, 2003, 09:53:29
Job time: 15.534 secs

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7 homo sapien
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[4] SEQUENCE FROM N.A. (ISOI TISSUE-Neuroblastoma; MEDLINE-99021697; PubMed De Laurenzi V. Costanzo Annicchiarico-Petruzzell "Two new p73 splice vari transcriptional activity Exp. Med. 188:1763-175] Exp. Med. 188:1763-175] SEQUENCE FROM N.A. (ISOI TISSUE-Breast cancer, He MEDLINE-99310938; PubMed De Laurenzi V. Catani P. (Costanzo A., Levrero M., "Additional complexity and identification of two	HUMAN 50; O15 CT-2001 CT-2001 CT-2001 CT-2003 R prote ein) OR P73 Sapien TYOTE R TYOTE	134.5 129.5 129.5 128.5 128.5 128.5 128.5 128.5 126.5 126.5 126.5
Complexity	STANDARD; 5351; Q9NTK8; 11 (Rel. 40, Cr 11 (Rel. 42, Ca 13 (Rel. 42, La 13 (Rel. 42, La 13 (Rel. 42, La 14 (Rel. 42, La 15 (Rel. 42, La 16 (Rel. 42, La 17 (Rel. 42, La 18 (Re	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
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GAMMA A 2988; Barcaro Levrer , gamma 998). EPSILON EPSILON B1648; Terrino Terrino ght R.A. 3: induc	ARD; PRT; (8; Created) Last sequence Last sequence Last sequence Last annotati 33-like transcr Crani C	NBL DI NAP3 J NE4 J NOSA J NACKA NAC
AND DELTA). roli D., Terrinoni ero M., Melino G.; a and delta, with o non AND ZETA). ON AND ZETA). mphocytes, and Skir noni A., Corazzari A.; and smitogens cing variants epsil	update) update) on update) iption factor) (p iption factor) (p intion factor) (p int	ABL_DROME ZAP3_MOUSE TLE4_MOUSE TCR_TEMPO YOR_TEMPO YOR_TEMPO TUSP_HUMAN TUSP_HUMAN GALY_YEAST YOK_TYMVA STUA_EMENI K167_HUMAN V70K_TYMV ALIGNMENTS
n ff	-rela telec omo. -C., P., M P., M ncers	P00522 09r017 Q62441 074522 074727 09nrj4 09nrj4 P19659 P19659 P20131 P36013 P10357
Falco M., erent Melino G., Melino G., lymphoid cells	lated sostomi; valent A., McKeon F., region region re; riwara K.,	mus musculu mus musculu schizosacch turnip yell homo sapien homo sapien saccharomyc turnip yell emericella homo sapien

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"Solution structure of a conserved C-terminal domain of structural homology to the SAM domain.";
EMBO J. 18:4438-4445(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF 439-506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99217940; PubMed=10203277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kharbanda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 399:814-817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yuan Z.-M., Si
Kharbanda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (ISOFORMS ALPHA AND BETA)
MEDLINE=99318135; PubMed=10391251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM KAPPA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Death Differ. 6:389-390(1999).
[6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99380160; PubMed=10449409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaelin W.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl.
        TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER, SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
INDUCTION: NOT INDUCED BY DNA DAMAGE.
INDUCTION: NOT INDUCED BY DNA DAMAGE.
DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERWINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.
TO THE ABL TYROSINE KINASE SH3 DOMAIN.
DISEASE: MAPS TO A CHROMOSOME REGION TO BE FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN NEUROBLASTOMA AND OLIGODENDROGLIONA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE TYPOSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPIC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMA INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IUm.
I Z.-M., U
NEUROBLASTOMA AND OF SIMILARITY: BELONGS
                                                                                                                                                                       Name=Kappa;
                                                                                                                                                                                                                                                          Name=Epsilon;
IsoId=O15350-5;
                                                                                                                                                                                                                                                                                                                                              Name=Gamma;
IsoId=O15350-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTS WITH ISOFORM GAMMA, ALPHA, SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                         Name-Beta
                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   emerging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    original reading f
                                                                                                                                                                                                                           Note=The splicing original reading f
                                                                                                                                                                                                                                                                                                                Note=The splicing of ex original reading frame;
                                                                                                                                                           IsoId=015350-7;
                                                                                                                                                                                   IsoId=015350-6; Sequence=VSP_006546;
                                                                                                                                                                                                                                                                                        IsoId=01
                                                                                                                                                                                                                                                                                                                                                                        IsoId=015350-2;
                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=015350-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400:792-792(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shioya H., Ishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p53 gene
                                                                                                                                                                                                                 frame
                                                                                                                                                                                                                                                                                     5350-4; Sequence=VSP_006542,
                                                                                                                                                                                                                 ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ៩
                                                                                                                                                                                                              Sequence=VSP_006544, VSP_006545; sequence=VSP_006544, VSP_006545; ng of exon 11 results in a frameshift from the farme. The splicing of exon 13 reverts the the sequence of isoform Alpha;
                                                                                                                                                                                                                                                                                                                               sequence=VSP_006540,
ng_of exon 11 results
                                                                                                                                                        Sequence=VSP_006538;
                                                                                                                                                                                                                                                                                                                                                                        Sequence=VSP_006539;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91:594-598(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishiko T., Sun X., paum R., Kufe D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ databases
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
G
                                                                                                                                                                                                                                                                                    VSP_006543;
                                                                                                                                                                                                                                                                                                                             VSP_006541; in a frames
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;
                                                                                                                                                                                                                                                                                                                               frameshift from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huang Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RACTS HOMOTYPICALLY
ISOFORM GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Υ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p73 with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lu H.,
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DOMAIN
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                                                                                      DOMAIN
DOMAIN
                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                            Pfam; PF00870; P53; 1.
Pfam; PF00536; SAM; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOm; PD002681; P53; 1.
                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                     EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                           VARSPLIC
                                                                                                                                                                                                                                                GO: GO:0003700; F:transcription factor activity; TAS.
GO: GO:0008630; P:induction of apoptosis by DNA damage; TAS
GO: GO:0006298; P:mismatch repair; TAS.
                                                                                                                                                                                                                                                                                                  PDB; 1COK; 17-AUG-99.
PDB; 1DXS; 08-AUG-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                    VARSPLIC
                                                                                                                 DOMAIN
                                                                                                                                          DOMAIN
                                                                                                                                                   Apoptosis; Nuclear 3D-structure.
                                                                                                                                                                    Transcription regulation;
                                                                                                                                                                             PROSITE; PS00348; P53;
                                                                                                                                                                                                                               InterPro; IPR001660;
                                                                                                                                                                                                                                                                                 Genew; HGNC:12003; TP73.
                                                                                                                                                                                                                                                                                            TRANSFAC; T04931;
                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                     MOD_RES
                                                                              DOMAIN
                                                                                                                                                                                                                                        InterPro; IPR002117;
                                                                                                                                                                                                                                                                           MIM; 601990;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AF077625;
AF077626;
AF077627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF077620;
AF077621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF077628;
AF077616;
AF077617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y11416; CAA72220.
Y11416; CAA72221.
Y11416; CAA72219.
                                                                                                                                                                                                                                                                                                                      AL1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF077619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF077618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF077624;
                                                                                                                                                                                    SM00454;
                           495
                                                                    287
346
168
391
483
131
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AAC61887.1;
AAC61887.1;
AAC61887.1;
AAC61887.1;
AAC61887.1;
AAC61887.1;
AAC61887.1;
AAC61887.1;
                                                                                                                                                                                     SAM;
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AAC61887
                                                                                                                                                                                                                                                                                                                      CAB92742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC61887
                                                                                                                                                                                                                                                                                                                                               AAD39696.1;
                                                                                                                                                           protein;
                          636
                                                                    46
304
435
171
171
171
171
171
194
486
310
                                                    282
                                                                                                                                                                                                                                SAM.
                                                                                                                                                                    Activator; DNA-binding; Anti-oncogene;
                                                                                                                                                                                                                                                                                                                            JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED.
                                                                                                                                                           Phosphorylation;
                                                                                      POLY-GLN.
POLY-PRO.
        /FT1d-VSP_006538.
SFLTGLGCPNCIEFTGQGLQSIYHLQNLTIEDLGALKIPE
GYRWTIWRGLQDLKOGHDYSTAQQLLRSSNAATISIGGSGE
LQRQRVMEAVHFRVRHTITIPNRGGPGGGPDEWADFGFDLP
                                                                     PHOSPHORYLATION
                                                                              DNA-BINDING
                                                                                                      ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
MEDIATES OLIGOMERIZATION (POTENTIAL).
POLY-PRO.
                                                                                                                                          TRANSACTIVATION (BY SIMILARITY).
                                            isoform Kappa
                                                   GNTRCRHWVLCGDRGLSRPVLQGPSG
                                                                   (POTENTIAL).
TION (BY ABL)
                                                                                                                                                           Alternative
                                                                     (IN ISOFORM
                                                                                                                                                            splicing;
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Query Match
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Matches 283
                                                                                                                                                               Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                            O9XSK8; O9TSQ9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor protein p73 (p53-like transcription factor) (p53-related
                                                                                                                                                                                                                                                                                                                                                                                      TP73 OR P73.
                                                                                                                                                                                                                                                                                                                                                                                                  protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P73_CERAE
                                                                                                                                                                                                                                                              TISSUE-Kidney;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                        (BY SIMILARITY).
SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS
TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HO
AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
                                    Name-Beta
                                                                             Event-Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                IsoId=Q9XSK8-1;
                    IsoId=Q9XSK8-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVTDVVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--TSIKKRRSPDDELLYLPVRGRETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTEFTTILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGRDRKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSYDAQSSTEDALSPSPAIRSNTDYPGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPPLSMPSTSHCTPPPPYPTDCSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMNKLPSVNQLVGQPPPHSSAATPNLGPVGPG----MLNNHGHAVPANGEMSSSHSAQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMNKLPSVSQLIN---PQQRNALTPTTIPDGMGANIPMMGTH---MPMAGDMNGLSPTQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EILMKLKESLELMELVPQPLVDSYRQQQQ-----LLQRPSHLQ-PPSYGPVLSPMNKVHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVRGRENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAE
    POSSESES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMVSGSHCTPPPPPHADPSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                            (ISOFORMS ALPHA AND BETA).
 ; Sequence-VSP_006537; an ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.8%;
                                               Sequence=Displayed
                                                                             splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1415.5; DB 1;
Pred. No. 1.7e-89;
0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                              Named isoforms=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637
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                                                                                                                                                     TO THE ABL
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P53_ONCMY
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Best Local :
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 P53_ONCMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y11419; CAA72224.1; -. EMBL; Y11419; CAA72225.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT TO THE ABL TYROSINE KINASE SH3 DOMAIN.
-I- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; 015350; 1COK.
InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                      420
                                                                                                                                                                                                                              318
                                                                                                                                                                                                                                                            306
                                                                                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 LLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                      GVNKLPSVNQLVGQPPPHSSAATPNLGPVGSG----MLNNHGHAVPANSEMTSSHGTQ--
                                                                                                                                                       SMNKLPSVSQLIN--PQQRNALTPTTIPDGMGANIPMMGTH---MPMAGDMNGLSPTQAL
                                                                                                                                                                                                  EILMKLKESLELMELVPQPLVDSYRQQQQ-----LLQRPSHLQ-PPSYGPVLSPMNKVHG
                                                                                                                                                                                                                            EMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMN-
                                                                                                                                                                                                                                                            EDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGPGVKKRRHGDEDTYYLQVRGRENF
                                                                                                                                                                                                                                                                            EDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--TSIKKRRSPDDELLYLPVRGRETY
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                                                                             SMVSGSHCTPPPPYHADPSLV
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   STANDARD;
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63.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1408.5;
Pred. No. 5.1
   PRT;
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PIR; JH0631; JH0631.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            de Fromentel C.C., Padkel F., Chapus A., Baney C., May P., Soussi T.;
"Rainbow trout p53: cDNA cloning and biochemical characterization.";
Gene 112:241-245(1992).
-I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ratinopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00870; P53;
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01-MAY-1992 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P25035;
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
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SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no war
        227
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                                                                                                                                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                     169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR00386; P53SUPPRESSR.
                                                                                                                                                                                            LYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAP
                                                                                                                                                                                                                                                                                                          VTAPSPYAQPS-STFDALS-PSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long and this statement is not removed.
ILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQ----VSDSTKNGDGTKRP
                                                                                                          PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRP
                                                                                                                                                                LFCQLAKTCPVQIVVDHPPPPGAVVRALAIYKKLSDVADVVRRCPHHQSTSENNEGP-AP
                                                        RGHLVRVEGNQRSEYMEDGNTLRHSVLVPYEPPQVGSECTTVLYNFMCNSSCMGGMNRRP
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44 TRANSCRIPTION ACTIVATION (ACIDIC)
281 BY SIMILARITY.
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392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Activator
                                                                                                                                                                                                                                                                                                                                                                                                            Score 839.5; DB 1
Pred. No. 2.2e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY SIMILARITY).
8422250765545A1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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MBL outstation -
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Similarity

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Mismatches No. 4.6e-49

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P53_BARBU
Q9W678;
                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Evolutionary conservancy of p53 gene sequences in fish.";
"Evolutionary conservancy of p53 gene sequences in fish.";
"Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last
28-FEB-2003 (Rel. 41, Last
Cellular tumor antigen p53
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HSSP; P04637; 1
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Bhaskaran A., May D., Rand-We
"Evolutionary conservancy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinopterygii; Neopterygii; Cyprinidae; Barbus.
                                                                                                       SEQUENCE
                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                       DNA_BIND
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                  Nuclear protein;
                                                                                                                                                                                                                                                                                                                Anti-oncogene; DNA-binding;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).

SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
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                                                                                                                                                                                                                                                                                                                                                                                            PR00386; P53SUPPRESSR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                537; 1TUP.
IPR002117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD34212.1; -.
                                                                                                                                                                                                         Phosphorylation; Apoptosis
28 TRANSCRIPTION ACTIVATION
256 BY SIMILARITY.
329 OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40, Last sequence update)
41, Last annotation update)
tigen p53 (Tumor suppressor
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365
292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   P53.
                        33.4%;
                                                                                                          MW;
                                                                                                                                                                                                                                                                                                             Transcription regulation; Activator,
                                                                                                                               BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Craniata;
Teleostei;
                                                Score 819.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                      DB 1;
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                                                   Length 369;
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RESULT
P53_BRA
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97344388; PubMed-9200835;
Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
"Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA expression during embryogenesis.";
wal Mar. Biol. Biotechnol. 6:88-97(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53_BRARE STANDARD; PRT; 373 AA. P79734; Q90440; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor TP53 OR DRP53.
                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions must be proposed institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Winge
                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                              expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
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AAB40617.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h) (Danio rerio).
a; Craniata; Verte
; Teleostei; Osta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338
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Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                    similarity).
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                                                                                                                                                                                           ugh a collaboration -
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RESULT 6
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Best Local S
Matches 171
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MOD_RES
SEQUENCE
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DOMAIN
DOMAIN
MEDIINE-99071979; PubMed-9854815;
Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
"Identification and characterization of the tumor suppressor p53 in channel catfish (Ictalurus punctatus).";
Comp. Biochem. Physiol. 120B:675-682(1998).
-!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of
                                                                                                                                                                                                                                                               P53_ICTPU STANDARD; PRT; 376 AA. 093379; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor TP53 OR P53.
                                                                                                                                                                                                  Ictalurus punctatus (Channel catfish).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii, Neopterygii; Teleostei;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD002681; P53; 1
PROSITE; PS00348; P53; 1
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ZFIN; ZDB-GENE-990415-270;
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein; Phosphorylation; Apoptosis.
DOMAIN 1 31 TRANSCRIPTION ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                       286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETRDGQVLGRRCFEARICACPGRDRKADEDSIRK-QQVSDSTKNGDGTKRPFRQNTHGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGNQRANYREDNITLRHSVFVPYEAPQLGAEWTTVLLNYMCNSSCMGGMNRRPILTIITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCPVQMVVDVAPPQGSVVRATAIYKKSEHVAEVVRRCPHHE--RTPDGDNLAPAGHLIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P--QPST----LPPTSTVPETSDYPGDHGFRLRFPQSGTAKSVTCTYSPDLNKLFCQLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNDSQ-EFAELWEKNLIIQPPGGGSCWDIIN--DEEYLPGS----FDPNFFEN-VLEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA97408.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). PHOSPHORYLATION (BY SIMILARITY).

AC7AB724FA6B61FF CRC64;
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OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 806.5;
                                                                                                                                                                                                                      Ostariophysi;
                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6e-48;
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                                                                                                                                                                                                                                                                                 p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97;
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                                                                                                                                                                                                                       Siluriformes;
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ID P53 XEN
ID P5 P5
AC P5
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DT 2
DT 2
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P53_XEN
P07193;
  Xenopodinae; Xeno
NCBI_TaxID=8355;
[1]
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                                                                       Eukaryota; Metazoa; Chordata
Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                 Cellular
                                                                                                                               Xenopus laevis (African clawed frog)
                                                                                                                                                                                                         01-APR-1988
28-FEB-2003
                                                                                                                                                                                                                                                           01-APR-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P04637; 1TUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF074967; AAC26824.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                             XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activated genes ptosis induction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and FAS antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTCPVLMAVSSSPPPGSVLRATAVYKRSEHVAEVVRRCPHHERSNDSSDGP-APPGHLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                       ASKKSKNSSSDDEIYTLQVRGKERYEFLKKINDGLELSDVVPPADQEKYRQK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGNSHAQYVEDPITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETQDGHLLGRRTFEVRVCACPGRDRKTEESNFKKQQ-EPKTSGKTLTKRSMKDPPSHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGNSRAVYQEDGNTQAHSVVVPYEPPQVGSQSTTVLYNYMCNSSCMGGMNRRPILTIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDMLQPQSS--SSPPTSTVPVTSDYPGLLNFTLHFQESSGTKSVTCTYSPDLNKLFCQLA
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347
286
375
376
                                                                                                                                                                                                      3 (Rel. 07,
3 (Rel. 07,
3 (Rel. 41,
                                                                                                       Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                  Xenopus
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                                                                                                                                                                              antigen
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation; Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41989 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.4%;
                                                                                                                                                                              Last sequence update)
Last annotation updat
n p53 (Tumor suppresso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is an inhibitor of cyclin-dependent kinases. seems to be mediated either by stimulation o expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; Activator;
                                                                            Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 795; DB 1;
Pred. No. 2.2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE PHOSPHORYLATION (BY SIMILARITY).
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                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1B89CD98DB3289F2 CRC64;
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                                                                                                                                                                            tion update)
                                                                                                                                                                                                                                                                                                             363
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                                                                                                                                                                              p53).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                            Pipidae;
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Matches 151
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CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soussi T., de Fromentel C.C., Mechali M., May P., Kro
"Cloning and characterization of a cDNA from Xenopus
for a protein homologous to human and murine p53.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M36962; AAA49923.1;
EMBL; X05191; CAA28821.1;
EMBL; X77546; CAA54672.1;
EMBL; S68353; AAC60746.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-94134403; PubMed-8302570;
Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.;
"Overexpression of wild type p53 interferes with normal development
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                    DNA_BIND
                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                 Nuclear
                                                                                                                                                                                                                                                                                                                                                               Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A29376; A29376.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The European Bioinformatics Institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in Xenopus laevis embryos.
Oncogene 9:109-120(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=88143684; PubMed=2830576;
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                         Local 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
             188
                                                                                                                                                   Similarity 54.5
51; Conservative
                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                         PR00386; P53SUPPRESSR.
GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFE
                                          GSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYMEDVNS
                                                        GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT
                                                                                              SCAVPSTDDYAGKYGLQLDFQQNGTAKSVTCTYSPELNKLFCQLAKTCPLLVRVESPPPR
                                                                                                            SPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit
                                                                                                                                                                                                           363
                                                                                                                                                                                                                                                                                                       Phosphorylation, Apoptosis.
TRANSCRIPTION ACTIVATION
BY SIMILARITY.
331 OLIGOMERIZATION.
                                                                                                                                                                                                                                      267
331
356
293
362
71
                                                                                                                                                                                                            40692
                                                                                                                                                                  31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . . . . .
                                                                                                                                                                                                            ₩;
                                                                                                                                                     42;
                                                                                                                                                   Score 762; DE
Pred. No. 3.9e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Transcription regulation;
                                                                                                                                                                                                                  MISSING (IN REF.
                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY SIMILARITY).
T -> S (IN REF. 2).
                                                                                                                                                                                                                                                                             BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                            CE1F3E58F020D74D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ng as its content is in ved. Usage by and for conventions
                                                                                                                                                   DB 1; I
8.9e-45;
les 68;
                                                                                                                                                                               Length 363;
                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kress
                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                    (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                               Activator,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration - MBL outstation
                                                                                                                                                     16;
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                                                                                                                                                   Gaps
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RESULT E
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                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 EMBL; AF098067; AAF04620.1; HSSP; P04637; 1C26.
                                            DOMAIN
DOMAIN
                                                                                                                                             PRINTS; PR00386; P53SUPPRESSR ProDom; PD002681; P53; 2. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncogene 18:5005-5009(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P53_PIG
 MOD_RES
                                                                                                                                                                                     Pfam; PF00870; P53;
                                                                                                                                                                                                  HSSP; P04637; 1C26.
InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99422034; PubMed-10490836;
Burr P.D., Argyle D.J., Reid S.W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
28-FEB-2003
                            MOD_RES
                                                                                      DNA_BIND
                                                                                                   Nuclear protein; Phosphorylation; DOMAIN 1 45 TRANS
                                                                                                                               Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
"Nucleotide sequence of the porcine p53 cDNA, and the detection recombinant porcine p53 expressed in vitro with a variety of ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                        in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                   DISEASE: p53 is found in
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Binds DNA as a homotetramer (By similarity). SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAX and FAS antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis induction
                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187
                                                                                                                                                                                                                                                                                                                                                                                                     transformed cells. p53 is frequently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI |:|: | ::|| | :| | : :|| : | | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRVCACPGRDRRTEEDNYTKKRGLKPSGK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKRR---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRHSVCVPYEGPQVGTECTTVLYNYMCNSSCMGGMNRRPILTITLETPQGLLLGRRCFE
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1 (Rel. 40, Last s
3 (Rel. 41, Last s
                             94
318
361
304
  385
                                                                                                                              DNA-binding;
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                               285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seems to be mediated either by stimulation expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence update)
annotation update)
(Tumor suppressor
                                                                                                                             Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                   increased amounts
                                         BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                  TRANSCRIPTION ACTIVATION (ACIDIC)
PHOSPHORYLATION (BY SIMILARITY).
                            PHOSPHORYLATION
                                                                       OLIGOMERIZATION
                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Sus.
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                                                                                                                             Activator
                                         (POTENTIAL).
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of anti-p53
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                                                                                                                                                                                                                                                                                                                                 collaboration
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RESULT 9
P53_CHICAG
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Matches
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                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 16:11383-11383(1988).

-I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BCl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P53_CHICK P10360;
  use by non-profit institutions as long a modified and this statement is not removed; entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cellular tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (Rel. 10, Creat
01-MAR-1989 (Rel. 10, Last
28-FEB-2003 (Rel. 41, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oncoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soussi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89083584; PubMed-3060861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPAFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a cDNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ьоса.
                                                                                                                                                                                                                    BAX and FAS antigen expression, or by repression of B expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEVVRRCPHHERSSDYSDG-LAPPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYEPPEVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.1%; Score 761.5; 45.3%; Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update) annotation update)
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01-NOV-1995 (Rel. 32, La
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Cellular tumor antigen p
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ProDom; PD002681; P53;
PROSITE; PS00348; P53;
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Felis silvestris catus (Cat).
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Fissipedia; Felidae;
                                              Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T., O'Brien S.J., Tsujimoto H., Hasegawa A.;
                                                                                     SEQUENCE OF 34-354 FROM N.A. MEDLINE=94114699; PubMed=8286534;
  suppressor
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PIR; S02193; S02193.
HSSP; P04637; 1TUP.
  "Molecular cloning
                                                                                                                                                                                         Watari T., Goitsuka R., Tsujimoto H., Hasegawa A. "Cloning of feline p53 tumor-suppressor gene and hematopoietic tumors.";
                                                                                                                                                                                                                                                           MEDLINE-94333960; PubMed-8056458;
Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y.,
                                                                                                                                                                                                                                                                                                            TISSUE=Lymph node;
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                                                                                                                                                                   58:602-607(1994).
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30 TRANSCRIPTION ACTIVATION
278 BY SIMILARITY.
339 OLIGOMERIZATION.
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                     and chromosomal mapping of feline
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Last annotation update)
n p53 (Tumor suppressor
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Pred. No. 6.8e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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DISEASE: p53 is found
of transformed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Acts as a tumor suppressor in many tumor types; induce growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation a a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAX and FAS antigen expression,
 292
                                                                                                                  173
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                                                                                                                                                                                                                                                                                          al Similarity
147; Conserv
                                                                                                                                                                                                       95
                                                                                                                                                                                                                                                                43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an email to license@isb-sib.ch).
                KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLEL
                                                                                                                                 PPPGSTKRALPPST - - - SSTPPQKKKPLDGEYFTLQIRGRERFEMFRELNEALEL
                                                                        NSSCYGGMNRRPILLIYTLETRDGQYLGRRCFEARICACPGRDRKADEDSIRKQQYSDST
                                                                                                                                                                            SVTCTYSPPLNKLFCQLAKTCPVQLWVRSPPPPGTCVRAMAIYKKSEFMTEVVRRCPHHE
                                                                                                                                                                                                       SATWIYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHE
                                                                                                                                                                                                                                   DDASGMSAVPAPAAPAPAT-----PAPAISWPLSSFVPSQKTYPGAYGFHLGFLQSGTAK
                                                                                                                                                                                                                                                              DHAQNSVTAPSPYAQPSSTFDALSPSPAI -----
                                                                                                                  RCPDSSDG-LAPPQHLIRVEGNLHAKYLDDRNTFRHSVVVPYEPPEVGSDCTTIHYNFMC
                                                          {\tt NSSCMGGMNRRPIITIITLEDSNGKLLGRNSFEVRVCACPGRDRRTEEENFRKKGEPCPE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                              385
285
386
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p53 is found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binds DNA as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10LG
                                                                                                                                                                                                                                                                                                                                                   Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                 385
285
42692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s found in increased amounts in a wide variety cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                         30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a homotetramer
                                                                                                                                                                                                                                                                                                                                                    ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear.
                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                            Score 753.5;
Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSCRIPTION ACTIVATION BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                       BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                 -> R (IN REF. 2)
D08B43BA1BC8EB78
                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis
                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Ву
                                                                                                                                                                                                                                                                                                          . 6e-44
                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
                                                                                                                                                                                                                                                              PSNTDYPGPHSFDVSFQQSSTAK
                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         PRPK)
                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ACIDIC)
                                                                                                                                                                                                                                                                                                                        386;
                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              induces
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       commercia]
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RESULT 11 P53_TETMU

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                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Evolutionary conservancy of p53 gene sequences in fish.";
Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
-I-FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P53_TETMU
Q9W679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF071571; AAD34213.1; HSSP; P04637; ITUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cellular tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bhaskaran A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon miurus (Congo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=94908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                              127
                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                         148;
                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD002681; P53; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                       QPSSTEDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
                                              SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR
                                                                                                                                         IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN
                                                                                                                                                                                                                    EPPSRDGANSSSPTVPVTTDYPGEYGFKLRFQKSGTAKSVTSTYSEILNKLYCQLAKTSL
ERAQYFEHPHTKRQSVTVPYEPPQLGSEFTTILLSFMCNSSCMGGMNRRPILTILTLETQ
                                                                                                           VEVLLGKDPPMGAVLRATAIYKKTEHVAEVVRRCPHHQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  May D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation;
47 TRANS
                                                                                                                                                                                                                                                                                                                                                              30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     41266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rand-Weaver M., Tyler C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    puffer)
                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                             Pred. No. 5.7e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
PHOSPHORYLATION (BY SIMILARITY).
ACC10EEE2F5F9CFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                Score 745; DB 1;
Pred. No. 5.7e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                      76;
                                                                                                                                                                                                                                                                                                                                                                                     Length 367;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                           NEDSAEHRSHLIRMEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                Gaps
                                                    236
                                                                                                                                                             176
                                                                                                         181
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241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53_CANFA STANDARD; P1
Q29537; Q9TV78;
Q1-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last seque
28-FEB-2003 (Rel. 41, Last anno)
Cellular tumor antigen p53 (Tumo
                                                                                                                                                                                                                                                                                                                                                                                                                                 Kraegel S.A., Pazzi K.A., Madewell B.R., "Sequence analysis of canine p53 in the Cancer Lett. 92:181-186(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIP3) (Dog).
Cardis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Cranidae;
Fissipedia; Canidae;
                                                                           or send an
                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watari T., Hasagawa A., Tsujimoto H.;
"Aberrations of p53 tumor suppressor gene in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  veldhoen N., Milner J.;
"Isolation of canine p53 protein.";
full length canine p53 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TP53 OR P53
                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95323915; PubMed=7600529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 25-300 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Setoguchi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Leukocyte;
MEDLINE-98178696; PubMed-9519881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cumors in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Spleen;
                                                                                                                                                                                                                                                                                                          FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                              expression.
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivate
                                                                                                                                                                                                      in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length canine p53 protein.
gene 16:1077-1084(1998).
                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237
 AF060514; AAC16909.1; -. AB020761; BAA78379.1; -. S77819; AAB42022.1; -. P04637; 10LG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295
                                                                           requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                          and this statement is not removed.
                                                                                                                            non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKSKTASSAEEDNNEVYTLQIRGRKRYEMLKKINDGLDLLENKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKRRS-----PDDELLYLPVRGRETYEMLLKIKESLELMQYLPQ 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGIVLGRRCFEVRVCACPGRDRKTEETNSTKMQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DEC-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakai T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Okuda M., Minehata K., Yazawa M., Ishizaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t sequence up
t annotation
3 (Tumor supp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detailed characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     the region of exons 3-8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381
                                                                                                                                         There
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                                                                                                                          ere are no rest
as its content
                                                                                           http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                      mutated or inactivated
                                                                                                          Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
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                                                                                                            bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spontaneous
                                                                                                                                         restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339
                                                                                                                                                          a collaboration
                                                                                                        for
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                                                                                                            n no way
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RESULTY
P53_B0V
P59_P5V
AC Q2
DT Q1
DT Q1
DT Q1
DT Q2
DT C6
GN TFF
OS BC
OC EC
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Best Local
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Q29628;
Q1-NOV-1997
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DOMAIN
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DOMAIN
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ProDom;
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                                                        SPECIES-Bovine; TISSUE-Liver; MEDLINE-95352829; PubMed-7626789;
                                                                                                                                                                                                                                                        Bos
                                                                                                                                                                                                                                                                                                 Cellular
                       Dequiedt F.
"Nucleotide
                                                                                                                                                NCBI_TaxID=9913,
                                                                                                                                                                      Bovidae; Bovinae;
                                                                                                                                                                                         Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                             Bos indicus (Zebu).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                  01-NOV-1997
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002117;
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  taurus (Bovine), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 HLLQKQTSIQS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                         F.,
                                                                                                                                                                                                                                                                                             tumor antigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLDDRNTFRHSVVVPYEPPEVGSDYTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLDGEYFTLQIRGRERYEMFRNLNEALELKDAQSGKEPGGSRAHSSHLKAKKGQSTSRHK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSSPPPPNTCVRAMAIYKKSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENNAQTQFSEPQYTNL----GLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENNVLSSELCPAVDELLLPESVVNWLDE-----DSDDAPRMP--ATSAPTAPGP--APSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGRNSFEVRVCACPGRDRRTEEENFHKKGEPCPEPPPGSTKRALPPST---SSSPPQKKK
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381 AA;
                                                                                                                                                                                                                                                                                                                (Rel. 35, (Rel. 35, Rel. 35, Rel. 41,
                       , Kettmann R.
sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSSVPSPKTYPGTYGFRLGFLHSGTAKSVTWTYSPLLNKLFCQLAKTCPVQLW 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NA-binding; Transcription regulation; Activator; Phosphorylation; Apoptosis
                                                                                                                                                     9915;
                                                                                                                                                                      Bos.
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344
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                       the
Burny A., Willems L.,
he bovine P53 tumor-suppressor
                                                                                                                                                                                                                                                                                                                sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61;
                                                                                                                                                                                                                                                                                             (Tumor suppressor p53).
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TRANSCRIPTION ACTIVATION (ACIDIC)
BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 744; DB 1
Pred. No. 7e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARITY).
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                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        761A718FDC93DA59 CRC64;
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                                                                                                                                                                                         Ruminantia;
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                                                                                                                                                                                       Pecora;
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                       cDNA.";
                                                                                                                                                                                         Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
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Best Local
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                EMBL; U74450, ....
PIR; S51648; S51648.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X81704; CAA57348.1; -. EMBL; D49825; BAA08629.1; -. FMRI. IT74486; AAB51214.1; -.
                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                    proDom; pD002681; p53; 1.
proSITE; pS00348; p53; 1.
Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komori H., Ishiguro N., Horiuchi M., Shinagawa "Predominant p53 mutations in enzootic bovine "Pt. Immunol. Immunopathol. 52:53-63(1996).
                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                      DNA_BIND
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=Bovine; STRAIN=Holstein; MEDLINE=96401400; PubMed=8807776
                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                             Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 13-386 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Binds DNA as SUBCELLULAR LOCATION: DISEASE: p53 is found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of transformed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression
                                                                                                                 164;
                      65
                                             53
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                                                                                          σ
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                         PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5:261-264(1995).
TELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNE
                                                                    ELNVEPPLSQETFSDLWNLLPENNLLSSELSAPVDDLLPYTDVATWLDECPNE--APQMP
                                                                                         ENNAQTQFSEPQYTNLGLL----NSMDQQIQNGSSSTSPYN----TDHAQNSVTAP---
                      EPSAPAAPPPAT----PAPATSWPLSSFVPSQKTYPGNYGFRLGFLQSGTAKSVTCTYS
                                                                                                                                                          380
386
                                             -SPYAQPSSTFDALSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYS
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p53 is found
                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                             Phosphorylation; Apoptosis
                                                                                                                                                                                                        285
349
380
316
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380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            institutions as long as
                                                                                                                            41.5%;
                                                                                                                                     30.4%;
                                                                                                                                                               WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in increased amounts in a wide variety p53 is frequently mutated or inactivat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear
                                                                                                                 65;
                                                                                                                                                                                                                                                                                      Transcription
                                                                                                                                                                        Ø
                                                                                                                            Score 744; DB 1;
Pred. No. 7.1e-44;
                                                                                                                                                                                            BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
PHOSPHORYLATION (BY PRPK) (BY
SIMILARITY).
                                                                                                                                                                                                                                          TRANSCRIPTION ACTIVATION BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                         PHOSPHORYLATION (BY SIMILARITY).
R -> T (IN REF. 2).
                                                                                                                                                               222473F28C548F31 CRC64;
                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shinagawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                     regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukemic cell lines.";
                                                                                                                                     Length 386
                                                                                                                 Indels
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                                                                                                                                                                                                        (BY (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL
                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration
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16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, I
28-FEB-2003 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.; "Partial characterization of the woodchuck tumor suppressor, its interaction with woodchuck hepatitis virus X antigen in hepatocarcinogenesis."; Oncogene 15:327-336(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MARMO
InterPro; IPRO02117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                      EMBL; AJ001022; CAA04478.1; HSSP; P04637; lTUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marmota monax (Woodchuck).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cellular tumor antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                  in many types of cancer.
SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Binds DNA as a homotetramer (By SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                      DISEASE: p53 is found in
                                                                                                                                                                                                                                                                                                                                                                        expression
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                                                                                                                                                                                                                                                                                           transformed cells. p53 is frequently mutated many types of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPGESRAHSSHLKSK----KRPSPSCHKKPMLKR 380
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                      increased amounts in
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RESULT 15
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SEQUENCE
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                                                                                                                                                                                                                                                                                                            Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Cranilata; Pertebrata; Euteleos
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                            P53_ORYLA STANDARD; PRT; 352 AA. P79820; Q9PSU7; Q9PSU8; O1-NOV-1997 (Rel. 35, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 26-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last a
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DOMAIN
                                                                                          Gene
                       SEQUENCE FROM N. STRAIN-Himedaka;
                                                                                                          Krause M.K., Rhodes L.D., van Beneden R.J., "Cloning of the p53 tumor suppressor gene from (Oryzias latipes) and evaluation of mutational exposed fish.";
                                                                                                                                                                                                                                                                                                                                                                                                                              TP53 OR P53.
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Nuclear protein;
DOMAIN 1
                                                                                                                                                                                                    MEDLINE=97305153; PubMed=9161419;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=8090;
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                                                                                          189:101-106(1997).
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  Gumerlock P.H.,
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41.3%;
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                                              VARIANT THR-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 738.5; DB 1 Pred. No. 1.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY SIMILARITY). E1DE5DB84BA40182 CRC64;
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Wong J.T.Y.,
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  Hsieh
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                                                                                                                                      in MNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation of cDNAs encoding the p53 tumor suppressor gene in the Japanese Medaka (Oryzias latipes)."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF003949; AAD01195.1; -.
EMBL; AF003950; AAD01196.1; -.
HSSP; P04637; 1YCS.
HTTPTO; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.

ODMAIN

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48

TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00870; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                    297
                                                                                                                                     183 QLAQYFEDPYTKRQSVTVPYEPPQPGSEMTTILLSYMCNSSCMGGMNRRPILTILTLET-
                                                                    242
                                                                                    237 DGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSI 296
                                                                                                                                                                                                           128
                                                                                                                                                                                                                                             117
 288
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                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                 al Similarity
148; Conserv
KRKKSHSSGEEEDNREVFHFEVYGRERYEFLKKINDGLELLE 329
                              KKRRS-----PDDELLYLPVRGRETYEMLLKIKESLELMQ 331
                                                                                                                                                       SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR 236
                                                                                                                                                                                                      IQIKVMTPPPQGAVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN 176
                                                                                                                                                                                                                                                                            EPVPTNEVNPPPTTVPVTTDYPGSYELELRFQKSGTAKSVTSTYSETLNKLYCQLAKTSP
                                                                                                                                                                                                                                                                                                             QPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP 116
                                                                EGLVLGRRCFEVRICACPGRDRKTEEESRQKTQPK-----KRKVTPNT----SSS
                                                                                                                                                                                                                                                                                                                                                                                                                     352 AA;
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       87
302
334
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283
351
91
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                                                                                                                                                                                                                                                                                                                                                                 30.1%;
52.5%;
                                                                                                                                                                                                                                                                                                                                                 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Score 737.5; DB 1
Pred. No. 1.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                   196868A66351BFF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                                                                                               Length 352;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                               27;
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                                                                                                                                                                                                                                                                            127
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Search completed: August Job time: 10.1754 secs

7, 2003, 09:47:29

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                          Score
     2450
2443
24421
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
     100.0
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7:
9:
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115:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-538-106-17
2450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                        sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_archea:*
sp_bacteria:*
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sp_rodent:*
                                                                                                                                                                                           Length DB
    Q9UP26
Q9P184
Q9UBV9
Q9UBV9
Q9UBV9
Q99186
Q99186
Q99180
Q99181
                                                                                                                                                                                           ij
                                                                                                                                                                                                                          SUMMARIES
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Q9up26 homo sapien
Q9p1b5 homo sapien
Q9qwy9 mus musculu
Q9ubv9 homo sapien
Q9p1b4 homo sapien
Q9p1b4 homo sapien
Q9p1b6 rattus norv
Q75080 homo sapien
Q89097 mus musculu
Q991b7 homo sapien
Q9p1b7 homo sapien
Q9p1b7 homo sapien
Q9p1b7 rattus norv
Q9p1d8 rattus norv
Q9p1d8 rattus norv
Q9p1d8 homo sapien
Q9p1d8 homo sapien
Q9p1d8 homo sapien
                                                                                                                                                                                         Description
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45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
1217	1256	1256	1420.5	1435.5	1438.5	1442.5	1461.5	1489	1730.5	1766	1802	1802	1813	1816	1818	1826	1837	1868	1872	1884	1918.5	2077	2148	2303	2323	2323	2327	2342
49.7	51.3	51.3	58.0	58.6	58.7	58.9	59.7	60.8	70.6	72.1	73.6	73.6	74.0	74.1	74.2	74.5	75.0	76.2	76.4	76.9	78.3	84.8	•	•	•	94.8	95.0	95.6
232	514	426	587	450	631	590	641	284	365	483	487	470	487	588	576	457	389	393	356	393	501	471	416	582	680	663	680	680
4	1	4	4	4	11	11	13	11	13	11	11	11	4	13	13	13	11	11	4	4	4	4	4	13	11	11	11	4
Q96KR0	Q9CU77	Q8NHW9	Q8TDY6	Q8TDY5	Q9JJP2	Q9JJP1	Q9W664	Q8C826	Q988W0	088897	Q99JE0	Q99JE1	Q9H3D2	Q8JHZ6	Q8JFE3	Q8JHZ5	088899	Q99JD9	Q9UP74	075922	Q9H3P8	Q9NPH7	Q9P1B6	Q9DEC7	Q9JJP6	Q99ЛЕЗ	088898	Q9UE10
Q96kr0 homo sapien	7 mus		omo	Q8tdy5 homo sapien	Q9jjp2 mus musculu	Q9jjp1 mus musculu	Q9w664 barbus barb	Q8c826 mus musculu	Q98sw0 xenopus lae	O88897 mus musculu	Q99jeO rattus norv	Q99jel rattus norv	Q9h3d2 homo sapien			Q8jhz5 brachydanio	O88899 mus musculu	9 rat	Q9up74 homo sapien	homo	Q9h3p8 homo sapien	homo	homo sa	Q9dec7 gallus gall	rattus	Q99je3 rattus norv	O88898 mus musculu	Q9ue10 homo sapien

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Best Local S
Matches 461
                                                                                                                                                                                                                                                                                                                                                                                                       Q9P1B5;
Q9P1B5;
Q1-OCT-2000
Q1-OCT-2000
Q1-OCT-2002
   EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                       Tani M.,
Yokota J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00870; P53; 1. PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1. Nuclear protein.
                                                                                          EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                             Neoplasia 1:71-79(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR
-!- SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                   "Mutation and expression of the Neoplasia 1:71-79(1999).
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=20388515;
                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                    OCT-2000 (TrEMBLrel. 15, Created)
OCT-2000 (TrEMBLrel. 15, Last sequence up
OCT-2002 (TrEMBLrel. 22, Last annotation
isoform delNbeta.
 AF116762;
AF116763;
AF116764;
                                                      AF116760;
AF116761;
                                                                                        AF116769;
AF116758;
AF116759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                        Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIWQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
 BELONGS TO T

AAF43492.1;

AAF43492.1;

AAF43492.1;

AAF43492.1;

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Primates;
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Pred. No. 4.2e-199;
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Best Local
Yang A., Kaghad M., Gillett E., Flem Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, enco transactivating, death-inducing, and Mol. Cell 2:305-316(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR (B-1- SIMILARITY: BELONGS TO THE P53 FEMBL; AF075438; AAC62643.1; -.
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EMBL; AF116766; AAF43492.1;
EMBL; AF116767; AAF43492.1;
EMBL; AAF13767; TCS.
HSSP; P04637; TCS.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                   Q9QWY9;
01-MAY-2000
01-MAY-2000
01-OCT-2002
                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eukaryota; Eutheria; Rodentia;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                DN p63 beta. TRP63.
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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SEQUENCE 461 AA;
                                                                             SEQUENCE FROM N.A. MEDLINE=98448095;
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O (TrEMBLrel.)
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AAF43492.1;
AAF43492.1;
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Pred. No. 1
                                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
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                                       encodes multiple produce, and dominant-negative
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Interpro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOM; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
                                                                                                                                                            Q9UBV9
Q9UBV9;
Q1-MAY-2000 (
Q1-MAY-2000 (
Q1-OCT-2002 (
DN P63 alpha.
P63.
         SEQUENCE FROM N.A
Lee L.A., Walsh P
Dellavalle R.P.,
                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

WANDLINE=98448095; PubMed=9774969;

Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.

Randrews N.C., Caput D., McKeon F.;

"p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activity

Mol. Cell 2:305-316(1998).
                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                NCBI_TaxID-9606; [1]
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Pred. No. 3
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Chorzelski T.P.,
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SEQUENCE 586 AA; 65756
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-!- SIMILARITY: BELONGS THE STATE OF T
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Pfam; PF00870;
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AF124538;
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AF124533; AAG45610.
AF124534; AAG45610.
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AF124530; AAG45610.1;
AF124531; AAG45610.1;
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AF124536; AAG45610.
AF124537; AAG45610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P04637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1637; 1YCS.
; IPR002117; 1
; IPR001660; !
                                                                                                                                        DMNGLSPTQALPPPLSMPSTSHCTPPPPPYPTDCSIV
                                                                                                                                                                                                  SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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nilarity 100.0%;
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SAM.
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the EMBL/GenBank/DDBJ databases
. NUCLEAR (BY SIMILARITY).
TO THE P53 FAMILY.
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Pred. No. 1.7e-196;
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InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002881; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
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Nuclear [
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HSSP; P04637;
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Mammalia; Eutheria; Primates;
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P51 isoform
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LI; AF116759; AAF43491.1; JOINED.

BL; AF116759; AAF43491.1; JOINED.

LI; AF116761; AAF43491.1; JOINED.

LI; AF116761; AAF43491.1; JOINED.

LI; AF116763; AAF43491.1; JOINED.

LI; AF116764; AAF43491.1; JOINED.

BL; AF116765; AAF43491.1; JOINED.

LI; AF116766; AAF43491.1; JOINED.

LI; AF116766; AAF43491.1; JOINED.

LI; AF116766; AAF43491.1; JOINED.

LI; AF116766; AAF43491.1; JOINED.

LI; AF116768; AAF43491.1; JOINED.

LI; AF116768; AAF43491.1; JOINED.

LI; AF116768; AAF43491.1; JOINED.
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                                                                                  SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLLQKQTSIQ
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                      SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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                                                                     SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
                                                                                                                    LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                   YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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llarity 100.0%;
Conservative
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K., Kawahara C.,
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ProDom; PD002681; P53; 1
PROSITE; P500348; P53; 1
Nuclear protein.
SEQUENCE 461 AA; 5139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99JD6
Q99JD6;
Q1-JUN-2001
Q1-JUN-2001
Q1-CCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variants.";
FEBS Lett. 501:121-126(2001).
FEBS Lett. 501:121-126(2001).

-I- SUBCELLULAR LOCATION: NUCLEAR
-I- SIMILARITY: BELONGS TO THE P53
EMBL; AJ277453; CAC37105.1; -.
HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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MEDLINE-21363378; PubMed-11470269;
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"Identification and tissue distribution of novel KET/p63 splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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                  DMNGLSPTQALPPPLSMPSTSHCTPPPPPYPTDCSIVRIWQV
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                                                                                                                                                                                                 SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLLQKQTSIQ
                                                                                                                                                                                                                                                                                        LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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  DMNGLSPTQALPPPLSMPSTSHCTPPPPPYPTDCSIVRIWQV
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                                                                                    SQSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAG
                                                                                                                                                                             SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSMQ
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Last sequence up
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Pred. No. 2.2e-196;
""matches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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C -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
C -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
R EMBL; AB010153; BAA32433.1; -.
R HSSP; P04637; 1YCS.
R InterPro; IPR002117; P53.
R InterPro; IPR002117; P53.
R Pfam; PF00870; P53; 1.
R Pfam; PF00870; P53; 1.
R PFINTS; PR00386; P53; 1.
R PGOSITE; P8003454; SAM; 1.
R PGOSITE; PS00348; P53; 1.
W NUCLEAR TOOLEGARD.
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01-NOV-1998
01-OCT-2002
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075080;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Tanaka T., Shinkai Y., Kato H.;
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            DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
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                                                       SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                                                                   YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                           SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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2 (TrEMBLrel.
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99.3%;
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Pred. No. 4.6e-195;
1; Mismatches 2;
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Catarrhini;
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Best Local S
Matches 451
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Totalian Blohys. Res. Commun. 248:603-607(1998).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- SUBCIANTY: BELONGS TO THE P53 FAMILY.

EMBL; AB01013; BAA32432.1; -.

HSSP; P04637; 1YCS.

MGD; MGI:1330810; TTP63.

InterPro: IPR001660; SAM.

Pfam; PF00870; P53; 1.
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089097;
01-NOV-1998
01-NOV-1998
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01-NOV-1998 (TrEMBLrel. 0
01-OCT-2002 (TrEMBLrel. 2:
)N P63 alpha.
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ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                       Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transactivating, death-inducing, Mol. Cell 2:305-316(1998).
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MEDLINE=98448095; Pu
Yang A., Kaghad M.,
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SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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.., Gillett E., Fleming
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98.9%;
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or Mismatches 2;
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-I- SIMILARITY: BELONGS TO THE I
EMBL; ALZ77447; CAC37099.1; -.
HSSP; P04637; 1YCS;
Interpro; IPR001616; SAM.
Pfam; PF00870; P53; 1.
Pfam; PF00386; P53; 1.
PRINTS; PR00386; P53; 1.
SYART; SM0454; SAM; 1.
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O99JE2;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
DN KET alpha protein.
P63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00348; P53; 1.
Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Wistar; TISSUE-Tongue; MEDLINE-21363378; PubMed-11470269; Bamberger C., Schmale H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification and tissue distribution
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                                          YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                      VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                                   TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                                                                                                                                                                                                                                                                 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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                                                                                                                                                                                                                                      VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                   TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
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586 AA; 65732 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            97.5%;
98.5%;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2389; DB 11;
Pred. No. 8.6e-194;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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3 FAMILY.
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Best Local :
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SEQUENCE
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ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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289
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Q9H3D3; Q9UF27;
01-MAR-2001 (TrEMBLrel. 10
01-MAR-2001 (TrEMBLrel. 10
01-OCT-2002 (TrEMBLrel. 20
TA p63 beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: NUCLE
-i- SIMILARITY: BELONGS TO THE
EMBL; AF124539; AAG45608.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activit;
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-98448095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00870; P53; 1. PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hagiwara K.,
Submitted (J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L; AF124528; AAG45608.1; JOINED.
L; AF124529; AAG45608.1; JOINED.
L; AF124531; AAG45608.1; JOINED.
L; AF124531; AAG45608.1; JOINED.
L; AF124533; AAG45608.1; JOINED.
L; AF124534; AAG45608.1; JOINED.
L; AF124535; AAG45608.1; JOINED.
L; AF124536; AAG45608.1; JOINED.
L; AF124537; AAG45608.1; JOINED.
                                                                                                                                                                                                                                                                                                                   447;
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                                                                                                                                                                                                                                                                                                                                                                                               protein.
E 555 A
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                   PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                  PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                         TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                            TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                         PYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K., McMenamin M.G., Harris L.L., McMenamin M.G., Harris L.L., (JAN-1999) to the EMBL/GenBank/DDBJ databases (JAN-1999).
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                               62433 MW;
                                                                                                                                                                                                                                                                                                                                    97.1%;
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Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                    Score 2379; DB 4;
Pred. No. 5.6e-193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                               E22874BE7DBABCBE CRC64;
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dominant-negative activities.";
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; Homo.
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                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 11
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Best Local S
Matches 446
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-1- SUBCELLULAR LOCATION: NUCLEAR (BY
-1- SIMILARITY BELONGS TO THE P53 FAN
EMBL; AF116756, AAF43488.1; JOINED.
EMBL; AF116757, AAF43488.1; JOINED.
EMBL; AF116759, AAF43488.1; JOINED.
EMBL; AF116760, AAF43488.1; JOINED.
EMBL; AF116761; AAF43488.1; JOINED.
EMBL; AF116762, AAF43488.1; JOINED.
EMBL; AF116763, AAF43488.1; JOINED.
EMBL; AF116763, AAF43488.1; JOINED.
EMBL; AF116764, AAF43488.1; JOINED.
EMBL; AF116765, AAF43488.1; JOINED.
EMBL; AF116766, AAF43488.1; JOINED.
EMBL; AF116767, AAF43488.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9P1B7 PRELIMINARY;
O9P1B7;
O1-OCT-2000 (TrEMBLrel. 1:
O1-OCT-2002 (TrEMBLrel. 1:
O1-OCT-2002 (TrEMBLrel. 2:
P51 isoform TAp63beta.
                                                                                                                                                                                                                                                                    ProDom; PD002681;
PROSITE; PS00348;
Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE-20388515; PubMed-10935472;
Shimizu K., Kawahara C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mutation and expression of the p51 Neoplasia 1:71-79(1999).
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                                                                                                                                                                                                                                                                                       PR00386; P53SUPPRESSR
PD002681; P53; 1.
; PS00348; P53; 1.
                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                       26767,
637; 1YCS.
7, 1PR002117; P53.
70970; P53; 1.
853SUPPP
                                PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLLQKQTSIQSPSSYGNSSPPLNK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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PYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
                                                                                                                                                                                                                                                          516 AA;
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                          57598 MW;
                                                                                                                                                                                                 96.8%;
99.8%;
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15,
22,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                  0;
                                                                                                                                                                            Score 2372; DB 4; Length 516;
Pred. No. 2e-192;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                        07553781103738B1 CRC64;
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Query Match
Best Local Similarity
Matches 442; Conser
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Caput D., McKeon F.;

P63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities.";

Mol. Cell 2:305-316(1998).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE P53 FAMILY.

EMBL; AF075435; AAC62640.1; --

HSSP; P04637; IYCS.

MGD; MGI:1330810; Trp63.

InterPro; IPR002117; P53.
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Q9QWZ0;
01-MAY-2000
01-MAY-2000
01-OCT-2002
TA*P63 beta.
                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00336; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 555 AA; 62454 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRP63.
Mus musculus (Mouse).
Mus musculus (Mouse).
Theria; Rodentia; (Mouse).
Theria; Rodentia;
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MEDLINE=98448095; PubMed=9774969;
MEDLINE=98448095; PubMed=9774969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                       15 PQYTNLGLLNSMDQQIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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TDYPGPHSFDVSEQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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98.9%;
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Last sequ
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Pred. No. 5e-191;
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RESULT RESULT OF STATE OF STAT
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 441; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002117; p53.
Pfam; pF00870; p53; 1.
PRINTS; PR00386; p53SUPPRESSR.
PRODOm; pD002681; p53; 1.
PROSITE; PS00348; p53; 1.
Nuclear protein.
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Q99JD7;
Q1-JUN-2001
Q1-JUN-2001
Q1-OCT-2002
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MEDLINE-21363378; PubMed-11470269;
Bamberger C., Schmale H.;
"Identification and tissue distribution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i SUBCELLULAR LOCATION: NUCLE
-i SIMILARITY: BELONGS TO THE
EMBL; AJ2771452; CAC37104.1; -.
HSSP; P04637; IYCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus
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PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                     TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                                                                                     LSMPSTSHCTPPPPYPTDCSIVRIWQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 AA; 60326 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 22, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                              Score 2352; DB 11; Length Pred. No. 1e-190; Indels 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66D0CA19786BF21B CRC64;
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3 FAMILY.
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                  538;
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Best Local S
Matches 441
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Q99JD8;
01-JUN-2001
01-JUN-2001
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002117; p53.
Pfam; PF00870; p53; 1.
PRINTS; PR00386; P53SUPPRE
ProDom; PD002681; P53; 1.
                                                                                                                                                                                                                                                                                                                                 proDom; pD002681; P53; 1.
prOSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 555 AA; 62426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variants.";
FEBS Lett. 501:121-126(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ277451; CAC
HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: NUCLEAR
-i- SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21363378; PubMed=11470269; Bamberger C., Schmale H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Wistar; TISSUE=Tongue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272
                                                                                                                                                                                                                                                                      al Similarity 98.7
                                                                                                                                                                                                                                                                                                                                                                                              PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta
                                                                                                                                                                                                           TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                        PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                      PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAC37103.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                     96.0%;
98.7%;
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17,
22,
                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                      ; Score 2352; D; Pred. No. 1.1e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAR (BY SIMILARITY)
P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                   65D8854E2387C74C CRC64;
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hes 3;
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                                                                                                                                                                                                                                                                                                     DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                   Length
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; Murinae; Rat
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF116769; AAF43487.1; JC
EMBL; AF116756; AAF43487.1; JC
EMBL; AF116757; AAF43487.1; JC
EMBL; AF116757; AAF43487.1; JC
EMBL; AF116760; AAF43487.1; JC
EMBL; AF116761; AAF43487.1; JC
EMBL; AF116762; AAF43487.1; JC
EMBL; AF116763; AAF43487.1; JC
EMBL; AF116764; AAF43487.1; JC
EMBL; AF116765; AAF43487.1; JC
EMBL; AF116765; AAF43487.1; JC
EMBL; AF116766; AAF43487.1; JC
EMBL; AF116767; AAF43487.1; JC
EMBL; AF116768; AAF43487.1; JC
EMBL; AF116769; AAF43487.1; JC

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075195;
01-NOV-1998
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
P51 isoform TAP63ALPHA (P51B protein).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
                                                                                               PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 641 AA; 72019
                                                                                                                                                                                        PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                              InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfiam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osada M., Ohba M., Kawahara C., Ishioka C., Kar
Ikawa Y., Nimura Y., Nakagawara A., Obinata M.,
"Cloning and functional analysis of human p51,
functionally resembles p53.";
Nat. Med. 4:839-844(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=SKeletal muscle;
MEDLINE=98324755; PubMed=9662378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tani M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P04637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neoplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               okota J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutation and expression of the p51 gene eoplasia 1:71-79(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB016073;
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AAF43487.1;
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Score 2350; DB 4;
Pred. No. 2e-190;
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                              GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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                LSMPSTSHCTPPPPPYPTDCSIV 456
                                                                                               GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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Search completed: August Job time: 39.092 secs 7, 2003, 09:51:43

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: /SIDS1/gcgdata/ger
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length DB	length	- 88	ID	Description
_	2082	100.0	393	20	AAY05957	Human cell regula
N	2082	100.0	393	23	ABG95133	Human oncogené p5
ω	2082	100.0	393	23	ABG95139	Human oncogene p6
4	2011	96.6	448	20	AAY45246	Human p51 protein
ű	2011	96.6	448	20	AAY05955	Human cell regula
6	2011	96.6	448	21	AAB11359	Human p63 protein
7	2011	96.6	448	22	AAB82128	Human protein #1
8	2011	96.6	448	23	ABG95127	Human oncogene p5
9	2011	96.6	448	23	ABG95137	Human oncogene p51

. [0	2011	96.6	448	23	ABG95143	oncog
, <u> -</u> -	70TT	١٥) L	1 2	n rung cancer
2	2011	. 5	448	23	ABB74991	n p53 homolog
ω	2011	6	448	24	ABU56418	
4	2009	٠.	389	20	AAY05964	e cell regula
5	1938	ü	483	20	AAY05961	e cell regula
9	1884	0	416	23	ABG95130	n oncogene ps
[7	1884	0	461	21	AAB11362	p63 prote
80	1884	0	461	23	ABG95131	onc
9	1884	0	461	23	ABG95138	oncogene p6
õ	1884	٥.	461	23	ABP61914	lung
2	1884	٥.	461	23	ABB74994	p53 homolo
2	1884	٥.	586	20	AAY05956	cell regula
3	1884	0	586	23	ABG95132	Human oncogene p51
4	1884	0	586	23	ABG95140	oncogene p6
Š	1882	0	461	20	AAY05963	regula
9	1882		586	20	AAY05962	
27	1867	9	356	20	AAY43135	0
8	1867	9	356	21	AAB11360	
9	1867	9	356	23	ABP61912	φ
õ	1867	9	356	23	ABB74992	Human p53 homologu
7	1867	9	586	21	AAB11357	
2	1867	9	586	23	ABP61909	ρn
ä	1867	9	586	23	ABB74989	Human p53 homologu
4	1860	9	586	20	AAY41032	Human lung tumor a
š	1860	9	586	21	AAB11317	Human lung cancer-
9	1860	9.	586	23	ABP61869	Human lung cancer
37	1860	9.	586	23	ABB74949	tun
8	1813		471	23	ABG95129	gene p5
9	1813	7	471	23	ABG95134	ene
0	1813	7.	516	20	AAY05954	regula
Ξ	1813	.7	516	21	AAB11363	rotein
5	1813	7.	516	23	ABG95135	gene
ü	1813	7.	516	23	ABG95141	jene p6
4	1813	7.	516	23	ABP61915	0
ū	1813	7	516	23	ABB74995	Human p53 homologu

ALIGNMENTS

X	DR	DR	X	ΡI	XX	PΑ	×	PR	PR	XX	PF	X	PD	×	PN	×	SO	×	XΨ	ΚW	ΚW	×	DE	×	ΡŢ	×	AC	×	ij	AAYO	RESILT
	N-PSDB; AAX58576.	WPI; 1999-277595/23.		McKeon F, Yang A;		(HARD) HARVARD COLLEGE.			29-MAY-1998; 98US-0087216.		02-OCT-1998; 98WO-US21992.		22-APR-1999.		W09919357-A2.	·	Homo sapiens.		_	er; tumour suppressor; cell cycle conti	Cell regulatory protein; p63; hu-deltaNp63 beta; human;		Human cell regulatory protein p63, isoform deltaNp63 beta		16-AUG-1999 (first entry)		AAY05957;		AAY05957 standard; Protein; 393 AA.		T.P. 1

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CC dientify compounds useful for treating disorders involving such caches and caches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
                                   CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP 393
                                                                                                                                                                 SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
                                                                                                                                                                                                                                                                LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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                                                                                                                              SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
                                                                                                                                                                                                                                                                                                                                                                                                     YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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Pred. No. 1
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1.4e-182;
es 0;
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RESULT 2 ABG95133

ABG95133

standard; Protein;

393

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TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120

TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK

MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS

MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS

60 60 0

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Matches Query Match Best Local

Similarity

100.0%;

Score 2082; DB 23; Pred. No. 1.4e-182; Mismatches

Conservative

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Indels Length

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protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoletic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein HSP-90; rheumatoid arthritis; cancer; haematopoletic disorder; r cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML acute myeloid stic leukaemia; ALL; APL; NLL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                                                                                                                                                                                                                                                                                                                  cell population, treating proliferative diseases associated with protein or cellular protein isoforms (II) dependent on heat shock
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  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases, involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aberrations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genetically-defined disease associated with chromosomal ons yielding oncogenic fusion proteins, e.g. cell proliferative, involves administering an inhibitor of heat shock protein 90
393 AA;
                                          This is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 333-334;
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                                                                                                                                                                                                                                                                                                                                                                                                          describes a method of treating genetically-defined disease th chromosomal aberrations yielding oncogenic fusion treating cancerous cells containing (I) in a heterogeneous
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                                            amino acid
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                                          sequence of a human
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                                                                                                                                                                                                 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                           The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSD)-90, or selectively treating cells expressing (II) involving administering HSPO-inhibitor. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 9 HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute myeloid leukaemia; AML; ALL; APL, HHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
   oncogenic
                   treating
                                                                                                                                                          Disclosure;
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DB; ABS73331.
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              genetically-defined disease with chromosomal aberration yielding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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                                                                                                                                                          Page 345-346;
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   protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synovial sarcoma; viral infection.
                                                                                                                                                        389pp; English
treating cancerous
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                                                                                                                                Key
                                                                                                                                                                                                Human; p51;
                                                                                                                                                                                                                                                     07-JAN-2000
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                       WO9950412-A1
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142..321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
 Cell regulatory protein; p63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human p51 protein, which is related to p53 and has cell proliferation regulation and tumour suppression activity. The p51 gene can be used in the investigation, diagnosis and treatment of diseases such as cancer, with which the p53 family cell proliferation regulation is associated. The p51 protein may be used for screening potential agonists and antagonists of its regulatory function,
                      Human cell regulatory protein p63, isoform huTAp63 gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New p53 related human gene p51, useful for diagnosis, investigation treatment of cancers and screening for potential cell proliferation
                                              16-AUG-1999
                                                                    AAY05955
                                                                                         AAY05955 standard; Protein; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 147-148; 163pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-591318/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tor use as
                                                                                                                                                           375 KQSDVFFRHSKPPNRSVYP 393
                                                                                                                                                                                                                                       310
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                                                                                                                                                                                                                                                                                                                                                                                                                             15 PQYTNLGILNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSPYAQPSSTFDALSPSPAIPSN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                               GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                KQSDVFFRHSKPPNRSVYP 448
                                                                                                                                                                                          ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
                                                                                                                                                                                                     ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
                                                                                                                                                                                                                                     GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                             PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                           PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                   PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drugs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                            (first entry)
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 5.6e-176;
huTAp63 gamma; TAp63 gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 448;
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Best Local Similarity
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                                                                                                                                                                                         Sequence
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                                                                    75 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                  70
                      PVYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
                                                                                                              PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSPYAQPSSTFDALSPSPAIPSN
                                                       TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
          PYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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448 AA;

Conservative

0;

96.6%;

Score 2011; DB 20; Pred. No. 5.6e-176; Mismatches

Length Indels

0,

Gaps

0

134 129

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differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltaN form lacks the designated as deltaN and TA forms, where the deltaN form lacks the transactivation domain. The present sequence represents human p63 isotype TAp63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isotypes exist. Splice variants
                                    cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAV5953-64), polynucleotides (see AAV5957-64), polynucleotides (see AAV5957-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-277595/23.
N-PSDB; AAX58574.
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cell proliferation; cell differentiation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Fig 11; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated p63 cell regulatory protein for, e.g. treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-1998;
15-OCT-1997;
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transgenic animals.
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97US-0062076.
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Best Local Similarity
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
                                                                                                                                    This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-cells isolated from a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                      Sequence
                                                                                     are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
                                                                                                                                                                                                                                                                                                 Disclosure; Page 247-249; 261pp; English.
                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung in a patient -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-APR-2000; 2000WO-US08896
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ine; detection.
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)B; AAC66029.
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99US-0466396.
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2000US-0510376.
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 96.6%;
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                                                                                                                    WPI; 200
N-PSDB;
                                                               Chimera gene of the p53 family, useful for gene of cancer, comprises a transcription activating
                                                                                                                                                                         (IKAW/)
(SAKA )
                Example 1; Page
                                                 binding
                                                                                                                                                                                                                             09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                      Domain
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DB; AAF86588.
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                                                                                                                                                                                                                             99JP-0139034
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                  30-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..59
                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Transactivation_domain
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            57pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                  Oligomerisation_domain
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                                                                   therapy, and region and a
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429

374 369 314 309

treatment DNA

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RESULT 8
ABG95127
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AC ABG9
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DT 04-D
XX Chro
XX Chro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a chimera gene of p53 family encoding a transcription activating region, a DNA binding region, and an oligomer formation region of different p53 family proteins. The chimeric gene can be used for gene therapy of p53 variant human tumours, and analysis of the function of the p53 family gene. The present sequence was used in the
                                             01-MAR-2001; 2001US-272751P.
                                                                          01-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2002
               (CONF-)
                                                                                                         12-SEP-2002
                                                                                                                                                                    Homo sapiens
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RESULT 9
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ABG95137

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically defined disease with chromosomal aberration yielding treating genetically defined disease with chromosomal aberration yielding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
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         KQSDVFFRHSKPPNRSVYP
                                              ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating cancerous cells containing (I) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              describes a method of treating genetically-defined disease th chromosomal aberrations yielding oncogenic fusion
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Pred. No. 5.6e-176;
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04-DEC-2002 (first entry)

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CC protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) concept in the protein (HSP)-90, or selectively treating cells expressing (II) concept in the method is useful for treating genetically-defined disease with chromosomal aberration yielding concept in the terogeneous cell population, treating proliferative disease concept in the terogeneous cell population, treating proliferative disease concept in the terogeneous cell population, treating proliferative disease concept is or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. Concept) isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoletic disorder such as T or B cell (Imphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, cor a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rabbdomyosarcoma and concept in the method is also useful for treating viral confections. This is the amino acid sequence of a human oncogenic protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention describes a method of treating genetically-defined disease clated with chromosomal aberrations yielding oncogenic fusion sins (I), treating cancerous cells containing (I) in a heterogeneous population, treating proliferative diseases associated with mutant
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PYYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease

protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful in

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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABS73335
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                                                                                                                                                                       12-DEC-2000;
07-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer associated protein sequence SEQ ID NO:340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 AA;
                                                                                                                                         2001US-0850716.
2001US-0850778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                        Ą
                                                                                              CORP
                                        Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          lung
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100.0%;
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Pred. No. 5.6e-176;
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01-MAY-2002

(first entry)

Human p53 homologue isoform,

p63 (L530S)

protein

SEQ

ij

NO:340

ABB74991 standard; Protein; 448

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RESULT 12
ABB74991
ID ABB74
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AC ABB74
AC ABB74
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DT 01-MA
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DT 01-MA
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Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92146 and ABP61866 to ABP61992 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes isolated human lung carcinoma polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide detecting in the sample, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McNeill PD, Fanger
Carter D, Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel lung carcinoma polynucleotide sequences and polypeptides ence by the polynucleotides, useful in pharmaceutical compositions such vaccines and as markers to indicate the presence of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ϋ́ Z
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Pred. No. 5.6e-176;
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Cai F,
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Foy TM;
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12-DEC-2000;
07-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                       The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, tusion proteins, Teell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL4939 to ABL49300 and ABB74946 to ABB75970 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang T,
McNeill
Vedvick
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotides encoding lung
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02-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 322-323; 374pp; English
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DB; ABL49248.
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                                                                                                     PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                    TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang
          ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
                                                        GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                         PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                               PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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                                            GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
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2000US-0630940.
2000US-0643597.
2000US-0662786.
2000US-0685696.
2000US-0735705.
2001US-0850716.
                                                                                                                                                                                                                                                                              Conservative
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Fanger N, Retter MW,
Carter D, Watanabe Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US21065
                                                                                                                                                                                                                                                                                                                          AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                  96.68;
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Pred. No. 5.6e-176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor polypeptides, useful for treating
                                                                                                                                                                                                                                                                             Mismatches
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Marnerakis M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       response
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RESULT 13
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10-MAY-2001;
09-NOV-2001;
13-NOV-2001;
                                          methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. attelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56408-ABU56745 represent lung cancer associated
                                                                                                                                                                                   The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The
                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting a lung cancer-associated transcript in a cell from a patien for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aziz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasi small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2001;
12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lung
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                               polypeptides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EOSB-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer-associated polypeptide #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-093161/08.
DB; ABX76134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer-associated polypeptide; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375
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                                                                                                                                                                                                                                                                                                                                                                                   27; Page 196; 453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-284770P.
2001US-290492P.
2001US-339245P.
2001US-350666P.
2001US-350666P.
2001US-334370P.
2002US-372246P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       emphysema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      n a patient from the
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Sequence

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RESULT 14
AAYO5964
ID AAYO5964
ID AAYO5964
AC AAYO5
AC COLL
AAYO5
AC AAYO5
AC COLL
AAYO5
AC A
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Best Local
The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of protei which demonstrate certain sequence identity to known tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell regulatory protein; p63; mu-deltaNp63 gamma; mouse; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
                                                                                                Claim 23;
                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                          WPI; 1999-277595/23
                                                                                                                                                                                                                                                                                         McKeon F,
                                                                                                                                                                                                                                                                                                                                      (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse cell regulatory protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY05964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY05964 standard; Protein;
                                                                                                                                                                New isolated p63 cell regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-1998;
15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQSDVFFRHSKPPNRSVYP 393
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                                                                                                Fig
                                                                                                                                                                                                                                                                                       Yang
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                                                                                             20; 161pp;
                                                                                                                                                                                                                                                                                                                                                                                     98US-0087216.
97US-0062076.
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                                                                                             English.
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Pred. No. 5.6e-176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc identified by screening a cDNA library with a probe corresponding to exons 5-9 of p63. At least 6 different isotypes exist. Splice cc variants differing at the C-terminus are designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltan and TA forms, where the deltan form lacks the cc transactivation domain. The present sequence represents mouse p63 isotype mu-deltany63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent cartivities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Deltan isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. Cc fo3 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative compounds useful for treating disorders involving such considers, in detection and diagnosis, and in the production of processes, in detection and diagnosis, and in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       suppressor proteins p53 and p73. Mouse p63 cDNA was isol RACE. Sequencing of the amplification product indicated amplified cDNA possessed a truncated N-terminus, i.e. the transactivation domain was absent. Additional splice variances
                                                                                                        16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                  Mouse cell regulatory protein p63, isoform muTAp63 gamma
                                                                                                                                                                            AAY05961 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic animals.
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                                                                                                                                                                                                                                                                                 CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
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                                                                                                                                                                                                                                                                  CFRNELVEPRGEAPTQSDVFFRHSNPPNHSVYP
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Pred. No. 7e-176;
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Cell regulatory protein; p63; muTAp63 gamma; TAp63 gamma; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.

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                                                                                                                                                                                                                                                                                                                                                                    transactivation domain was absent. Additional splice variants were identified by screening a cDNA library with a probe corresponding to exons 5-9 of p63. At least 6 different isotypes exist. Splice variants differing at the C-terminus are designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltan and TA forms, where the deltan form lacks the transactivation domain. The present sequence represents murine p53 isotype muTAp63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivation of p63 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Deltan isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to processes, in detection and diagnosis, and in the production of
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Matches 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using RACE. Sequencing of the amplification product indicated that the amplified cDNA possessed a truncated N-terminus, i.e. the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. Mouse p63 cDNA was isolated usin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX58580
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15-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                              transgenic animals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McKeon F,
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97US-0062076.
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                 375 KQSDVFFRHSKPPNRSVYP 393
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Result
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Compugen Ltd.
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Sequence 343, App
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Sequence 338, App
Sequence 152, App
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Sequence 344, App
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SOFTWARE: FASTSEQ for Wi SEQ ID NO 340 LENGTH: 448 TYPE: PRT ORGANISM: Homo sapiens US-09-643-597-340

Best Loc Matches Query Match

Local

1ch 96.6%; Score 2011; DB 4; 1 al Similarity 100.0%; Pred. No. 1.3e-184; 379; Conservative 0; Mismatches 0;

Length 448; Indels

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Gaps

129

189 134

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PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV

255 250

GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP PYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV

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RESULT 1 US-09-643-59 Sequence Patent No Patent IN APPLICANY APPLI		2220000000000000000000000000000000000
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7-340 40, Applica 6426072 FORMATION: Fan, Li Kalos, J Hosken, Fanger, Fanger, Skeiky, Mang, A. Skeiky, Mang, A. Skeiky, Henderse, Hender		35. 35. 35. 35. 35. 35. 35. 36. 36. 36. 36. 36. 36. 36. 36. 36. 36
97-340 340, Applicatio 340, Ap		000000000000000000000000000000000000000
97-340 340, Application US/096 6426072 16426072 T: Wang, Tongtong T: Fan, Liqun T: Kalos, Michael D. T: Kalos, Michael D. T: Hosken, Nancy T: Hosken, Nancy T: Fanger Gary R. T: Li, Samuel X. T: Wang, Aijun T: Skeiky, Yasir A.W. T: Skeiky, Yasir A.W. T: Henderson, Robert F T: MCNeill, Patricia I T: MCNeill, Patricia I T: MCNEMTION: COMPOSITIC INVENTION: AND DIAGNU ERENCE: 210121.455C11 APPLICATION NUMBER: US, FILING DATE: 2000-08-2 F SEQ ID NOS: 369 F SEQ ID NOS: 369 F SEQ ID NOS: 369		4 @ W W W W W W W W W W W W W W W W W W
ion US/09643 gtong n chael D. haitanya S. lancy lary R. Ll X. Ll X		₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩
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o `	STN	975-3 975-3 975-3 580-2 5150-8 5150-8 5150-8 7021-17 70418-2 70418-2 70418-2 70418-2 70418-2 70418-2 70418-2 70418-2 70418-2 70418-2 70418-2 70418-2 70418-2
		9-277-196-20 9-281-975-3 9-281-975-3 9-257-580-2 8-307-1616-8 8-307-515A-8 8-307-515A-8 8-801-718-8 9-801-718-8 9-801-718-2 8-697-221-17 8-697-221-17 8-697-221-17 8-190-5160-6 8-347-792-2 8-390-5160-6 8-390-515A-6 8-390-515A-6 8-390-515A-6 8-390-515A-6 8-390-515A-6 8-390-515A-6
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RESULT 3
US-09-606-421B-340
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APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Comeounds and Methods for Invention: Comeounds and Methods for ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CA.
FILE REFERENCE: 210121.45508
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
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US-09-542-615A-340
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Best Local Similarity
Matches 379; Conserv
   Sequence 340, Application Patent No. 6531315
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100.0%; Pred. No. 1.3e-184;
tive 0; Mismatches 0;
                  US/09606421B
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CANCER
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APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION UNMBER: US/09/606,421B
NUMBER OF SEQ ID NO340
SEQ ID NO 340
LENGTH: 448
munn: Daniel Composition 3.0
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; TYPE: PRT
; ORGANISM: Homo s
US-09-606-421B-340
                                                                     GENERAL INFORMATION:
APPLICANT: Wang, To,
APPLICANT: Fan, Liq
APPLICANT: Kalos, M
APPLICANT: Bangur,
APPLICANT: Hosken,
APPLICANT: Fanger,
APPLICANT: Li, Samu
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Best Local Similarity
Matches 379; Conserv
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             APPLICANT:
   엵
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                                                                      Bangur, Chaitanya (Hosken, Nancy Fanger, Gary R. Li, Samuel X.
                                                                                                                                                                                                                                                                                                   KQSDVFFRHSKPPNRSVYP
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Henderson, Robert A.
McNeill, Patricia D.
VENTION: COMPOSITIONS
                                         Wang, Aljun
Skeiky, Yasir A.W.
                                                                                                                                  Kalos, Michael D.
                                                                                                                                                Wang, Tong
Fan, Liqun
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Pred. No. 1.3e-184;
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 AND
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   METHODS FOR
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374 369 314 309 254 249 194 189 134 129

Length 448; Indels

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Gaps

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THERAPY

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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens US-09-643-597-343
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Best Local S
Matches 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.
SEQ ID NO 343
LENGTH: 461
                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 343
                                   Query Match
Best Local Similarity
                      Matches
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                                                                                         ORGANISM: Homo
09-542-615A-343
                                                                                                                          TYPE: PRT
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                    Conservative
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                                   Score 1884; DB 4
Pred. No. 2e-172;
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                                                    DB 4;
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                                                    Length 461;
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APPLICANT: Wang, Aijun

APPLICANT: Skelky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C9

CURRENT APPLICATION NUMBER: US/09/606,421B

CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 343

LENGTH: 461

TYPE: PRT

ORGANISM: Homo sapiens
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Best Local S
Matches 361
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APPLICANT: Fan, I
APPLICANT: Kalos,
APPLICANT: Bangur
APPLICANT: Hosker
APPLICANT: Fanger
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181
                                                     121 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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                                                                                                        61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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                                 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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Fanger, Gary R.
Li, Samuel X.
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Pred. No. 2e-172;
3; Mismatches 7;
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APPLICANT: Skeiky, Tasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHOI
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG (
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION UNMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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US-09-643-597-341
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SEQ ID NO 341
LENGTH: 356
TYPE: PRT
ORGANISM: Homo sapiens
S-09-643-597-341
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Best Local
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             SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQK 355
                                                                         LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                  YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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Fanger, Gary R.
Li, Samuel X.
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                                                        {\tt LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPSRQNTHGIQMTSIKKRR}
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Fan, Liqun
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99.7%;
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Pred. No. 5.9e-171;
0; Mismatches 1;
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LUNG CANCER
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
FITILE OF INVENTION: COMPOUNDS AND METHODS
FITILE OF INVENTION: AND DIAGNOSIS OF LUNG C.
FILE REFERENCE: 210121,4556
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windown
SEQ ID NO 341
LENGTH: 356
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US-09-277-196-2
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LENGTH: 356
TYPE: PRT
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APPLICANT: Trink, Barry
APPLICANT: Jen, Jin
APPLICANT: Ratovitski, Edward
APPLICANT: Sidransky, David
TITLE OF INVENTION: p40 Protein Acts as an
FILE REFERENCE: 01107.79765
                                                                                                                                                                                                                                                                          Sequence 341, Application Patent No. 6518256
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Patent No. 6476206
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Best Local
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CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/079736
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 5.9e-171;
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APPLICANT: Skelky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.45509

CURRENT APPLICATION NUMBER: US/09/606,421B

CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 341

LENGTH: 356

TYPE: PRT
ORGANISM: Homo sapiens

US-09-606-421B-341
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US-09-606-421B-341
; Sequence 341, Application US/09606421B
natent No. 6531315
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitar
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R
APPLICANT: L1, Samuel X.
                                                                                                                                                        Query Match
Best Local Similarity
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VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                          TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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Bangur, Chaitanya S.
Hosken, Nancy
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Li, Samuel X.
                                                                                                                                          Conservative
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                                                                                                                                       Score 1867; DB 4; Length 356;
Pred. No. 5.9e-171;
0; Mismatches 1; Indels
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Pred. No. 5.9e-171;
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; SOFTWARE: FastSEQ for W:
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-338
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Best Local Similarity
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CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C11
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                                                                   LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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                                                    LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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Fan, Liqun
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Henderson, Robert A.
McNeill, Patricia D.
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Li, Samuel X.
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APPLICANT: Wang, Tonyoon,
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Cary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOF
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAI
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                                                                                                              Sequence 338, Application US/09606421B Patent No. 6531315
                                                                                                GENERAL
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Best Local Similarity
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                                  APPLICANT:
                                                                APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/542,615A CURRENT FILING DATE: 2000-04-14 NUMBER OF SEC ID NOS: 350
       APPLICANT:
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFDALSPSPAIPSNTDYPGPHSSDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLYLENNAQTQFSEPQYTNLGLLNSMDQQIRNGSSSTSPYNTDHAQNSVTAPSPYAQPSP
                                  Bangur, Chaitanya
                                                  Kalos, Michael D.
                   Hosken, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09542615A
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92.5%;
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Pred. No. 1.2e-170;
4; Mismatches 9;
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                                                         APPLICANT: Wang, Alju...

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: MCNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND ME'

TITLE OF INVENTION: AND DIAGNOSIS OF LU

TOP PREFERENCE: 210121.455C11
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Best Local Similarity
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 3.9
SEQ ID NO 152
                                                                                                                                                                                                                                                                                APPLICANT:
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
Kalos, Michael D.
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LUNG METHODS FOR

CANCER

THE

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APPLICANT: Li, Samuel ...

APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
                                                                                                                                                                                                                                                                                                                                                                      121 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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                                        CFRNELVEPRRETPKQSDVFFRHSKPP
                                                                                                       SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
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                                                                                                                                                               LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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-QTSIQSPSSYGNSSPP
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92.5%;
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                                        387
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RESULT 15
US-09-480-884A-152
; Sequence 152, Application US/09480884A
"arent No. 6482597
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; ORGANISM: Homo sapien
US-09-480-884A-152
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; ORGANISM: HOMO
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Best Local S
Matches 357
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CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
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Best Local Similarity
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APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
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                                                                                                                 al Similarity
357; Conserv
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TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                        MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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                                                                                                                89.3%; ilarity 92.2%; Conservative
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Pred. No. 5.9e-170;
Pred. No. 5.9e-170;
                                                                                                                Score 1860; DB 4;
Pred. No. 5.9e-170;
5; Mismatches 9;
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                                                                       VMTPPPQGAVIRAMPVYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                             SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA 360
                CFRNELVEPRRETPKQSDVFFRHSKPP 387
                                    SPDDELVYLPVRGRETYEMLVKIKESLELMQYLLQHTIETYRQQQQQQQHQHLLQK----
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QTSIQSPSSYGNSSPP 371
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Search completed: August 7, 2003, 09:54:56 Job time: 11.8414 secs (USPTO) XNALIB 32A9 SIHT

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Result
No.
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Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                 length: 0
length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US0C_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US0C_NEW_PUB.pep:*
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US-09-850-716A-341

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US-09-735-705-338

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Sequence 340, App
Sequence 340, App
Sequence 343, App
Sequence 343, App
Sequence 341, App
Sequence 341, App
Sequence 341, App
Sequence 341, App
Sequence 2, Appli
Sequence 338, App
Sequence 338, App
Sequence 338, App
Sequence 152, App
Sequence 152, App
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Sequence 28, Appl	 س د) .F	· (u		78	34	Sequence 2, Appli	'n	4	9	Sequence 4, Appli	9,	Sequence 3, Appli	32,	10	Ψ	20	19	34	æ	342	339	e 339	339, 🌶	344	æ	Sequence 344, App	152	2

ALIGNMENTS

RESULT 1 US-09-735-705-340

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Matches 379
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CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 340
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 340, Application US/09735705 Patent No. US20020052329A1
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                       APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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                                                                                         Local Similarity
                 15 PQYTNLGILNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
70
PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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Bangur, Chaitanya
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ilarity 100.0%;
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                                                                    Score 2011; DB 9;
; Pred. No. 3.4e-178;
0; Mismatches 0;
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APPLICANT: Kalos, Michael D.

APPLICANT: McNeill, Patricia D.

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION UNUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 340
                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-340
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US-09-850-716A-340
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                         ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLIQKHLLSACFRNELVEPRRETP
                                                                                GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                             PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                     PYYKKAEHYTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSYLV 194
                                                                                                                                                                                                                                              PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
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                                                                    GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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RESULT 4
US-09-735-705-343
; Sequence 343, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-340
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US-09-897-778-340
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SOFTWARE: FastSEQ for Windows Version SEQ ID NO 340
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APPLICANT: Warnerakis, Mar
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshi
APPLICANT: Handerson, Robe
APPLICANT: Peckham, David
APPLICANT: Panger, Neil
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Best Local Similarity
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
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Vedvick, Thomas
rter, Darrick
roshi)
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Pred. No. 3
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APPLICANT: KALOS, MICHAEL D.

APPLICANT: MCNEIL, PATTICIA D.

APPLICANT: MCNEIL, PATTICIA D.

APPLICANT: RELTEY, MARC W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C15

CURRENT APPLICATION NUMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 440

SOSTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 343

LENGTH: 461
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CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 343

LENGTH: 461

TYPE: PRT

ORGANISM: Homo Sapiens
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Best Local S
Matches 361
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Henderson, Robert A.
McNeill, Patricia D.
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Li, Samuel X.
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APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 343
LENGTH: 461
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                                                                                                                                    Query Match
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Best Local
                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                              APPLICANT: Peckham, David W.
APPLICANT: Franger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
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Pred. No. 2
                                                                                                 Score 1884; DB 10;
Pred. No. 2.2e-166;
3; Mismatches 7;
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US-09-735-705-341
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SEQ ID NO 341
LENGTH: 356
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Best Local
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
-09-735-705-341
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                  APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHO
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
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                                                                                                   TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                              MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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                                                                                       TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
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Skeiky, Yasir A.W.
Henderson, Robert A.
McNeill, Patricia D.
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Fan, Liqun
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Hosken, Nancy
Fanger, Gary R.
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Pred. No. 5.7e-165;
0; Mismatches 1;
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-850-716A-341
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 341
LENGTH: 356
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Best Local
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APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455CLS
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
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                     SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQK
                                                                                                                                                                               YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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                                                                                LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPSRQNTHGIQMTSIKKRR
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Pred. No. 5.7e-165;
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WESULT 9
US-09-897-778-341

Sequence 341, Application US/09897778
Patent No. US20020147143A1

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
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APPLICANT: Sidransky, David
FITTLE OF INVENTION: p40 Protein Acts as an On
FILE REFERENCE: 01107.79765
CCURRENT APPLICATION NUMBER: US/10/274,874
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: US/09/277,196
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 20
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US-10-274-874-2
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; ORGANISM: Homo sapiens
US-10-274-874-2
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Matches 354
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TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 341
LENGTH: 356
TYPE: DET
                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 356
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Best Local Similarity
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Matches 354;
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APPLICANT: Jen, Jin
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Pred. No. 5.7e
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CURRENT APPLICATION NUMBER: US/09/735,705; CURRENT FILING DATE: 2000-12-12; NUMBER OF SEQ ID NOS: 419; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 338; LENGTH: 586; TYPE: PRT; ORGANISM: Homo sapiens
US-09-735-705-338
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US-09-735-705-338
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APPLICANT:
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APPLICANT: Franger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
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SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQK 355
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Fan, Liqun
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Skeiky, Yasir A.W.
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Fanger, Gary R.
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92.5%;
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CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716A-338
                                                RESULT 13
US-09-897-778-338
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US-09-850-716A-338
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APPLICANT: Kalos, Michael D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
    GENERAL INFORMATION:
                 Sequence 338, Application US/09897778 Patent No. US20020147143A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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Pred. No. 1.2e-164;
4; Mismatches 9;
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US-09-735-705-152
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                                                                                                                                                                                                                   Sequence 152, Application US/09735705 Patent No. US20020052329A1
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CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 338
LENGTH: 586
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TITLE OF IN
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Best Local
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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   !: Fanger, Neil
INVENTION: COM
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                                                                                        Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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                         Wang, Aijun
Skeiky, Yasir A.W.
Henderson, Robert A.
McNeill, Patricia D.
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Fan, Liqun
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                                                                                                                                      Bangur, Chaitanya
                                                                                                                                                     Kalos, Michael D.
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Henderson, Robert A.
Peckham, David W.
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Vedvick, Thom
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   COMPOSITIONS
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Pred. No. 1.2e-164;
   AND
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   METHODS FOR THE
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300

THERAPY

Length 586; Indels

16;

Gaps

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; APPLICANT: Kalos, Michael D.
; APPLICANT: MCNeill, Patricia D.
; APPLICANT: MCNeill, Patricia D.
; APPLICANT: MCNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION UNUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTMARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ğ
                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-850-716A-152
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US-09-850-716A-152
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Best Local S
Matches 357
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CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 152, Application US/09850716A Patent No. US20020115139A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR 300
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                                                                    al Similarity
357; Conserv
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357; Conserv
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                  MLYLENNAQTQFSEPQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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nilarity 92.2%;
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                                                                                  89.3%;
92.2%;
                                                                Score 1860; DB 10;
Pred. No. 5.3e-164;
5; Mismatches 9;
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Pred. No. 5.3e-164;
5; Mismatches 9;
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                                                                                     YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV 240
             CFRNELVEPRRETPKQSDVFFRHSKPP 387
                                                                                                                 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPSSHLIRVEGNSHAQ
QTSIQSPSSYGNSSPP
371
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                                          360
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Search completed: August 7, 2003, 09:57:12 Job time: 17.7783 secs THIS PAGE BLANK (USPTO)

Perfect score: 2082 Sequence: 1 MIYLENNAQTQFSEPQYTNLPKQSDVFFRHSKPPNRSYYP 393 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283308 seqs, 96168682 residues Total number of hits satisfying chosen parameters: 283308

otal number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	. 19	18	. 17	16	15	14	13	12	11	10	9	8	7	σ	_C	4	ω	2	-	Result No.
98	98	86	99	99.5	100	102	104	104.5	104.5	104.5	104.5	108	109	109	111.5	259.5	687	698	700	700	703	707	712.5	720	745.5	758.5	762	839.5	Score
4.7	4.7	4.7	4.8	4.8	4.8	4.9	5.0	5.0			•	•	5.2	•	5.4	12.5	33.0	33.5	33.6	33.6	33.8	34.0	34.2	34.6	35.8	36.4	36.6	40.3	Query Match 1
1487	1144	751	1456	1203	628	947	2578	1912	1894	1703	1691	2529	4273	3942	1819	77	381	393	391	390	393	393	396	391	386	367	363	396	Length I
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			l Tod			hypothetical prote	transcription fact	protein-tyrosine-p	protein-tyrosine-p	SNF2 protein - yea	ne-	transcription fact	polyketide synthas	Bassoon protein -	hypothetical prote	cellular tumor ant	•		tumor suppressor p	cellular tumor ant	tumor	tumor	lular tumor	tumor	tumor	tumor	tumor	or a	Description

RESULT 2 A29376

40	44	43	42	41	40	39	3 8	37	36	35 5	34	ω	32	31	30
9	95	95	95.5	95.5	96	96	96	96	96	96	96	96.5	96.5	96.5	97
4.0	. 6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.7
979	490	466	2409	1505	1203	1106	890	890	890	628	427	1445	866	797	710
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SCETOS	T25147	A88868	A60979	JC4851	B55094	T31742	F72093	E81576	E86530	JQ0110	F85436	A59437	T45462	VGBEX1	T41586
пурослестскі ріосе	hypothetical prote	protein T23B5.3 [i	versican precursor	hypoxia-inducible	chromosomal protei	hypothetical prote	translation initia	translation initia	initiation factor-	hypothetical 69K p	hypothetical prote	KIAA1204 protein (membrane glycoprot	glycoprotein X pre	hypothetical serin

ALIGNMENTS

שמ 360	Qу 339	Oy 284	Qy 227 Db 240	Qy 167 Db 180	QY 107 Db 121	Qy 49 Db 61	Query Match Best Local : Matches 16	A;Cross-refe A;Experiment C;Comment: T C;Superfamil: C;Keywords: F;164,167,22 F;395/Bindin	JH0631 JH0631 Cellular tumor antigen C;Species: Oncorhynchus C;Date: 10-Sep-1999 #se C;Accession: JH0631 R;de Fromentel, C.C.; P Gene 112, 241-245, 1992 A;Title: Rainbow trout A;Reference number: JH0 A;Accession: JH0631 A;Molecule type: mRNA A;Residues: 1-396 < DEF>	מספווו ח ו
0 DKYROK 365	9 ETYRQQ 344	4 FRQ-NTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 338 ::: :	7 ILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRP 283 : ::	7 PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRP 226 : :: :	7 LYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREENEGQIAP 166 : : :	49 VTAPSPYAQPS-STFDALS-PSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKK 106	, Match 40.3%; Score 839.5; DB 1; Length 396; Local Similarity 55.2%; Pred. No. 2.6e-58; es 169; Conservative 47; Mismatches 79; Indels 11; Gaps 6;	A;Cross-references: GB:M75145; NID:g213828; PIDN:AAAA9605.1; PID:g213829 A;Experimental source: liver C;Comment: This protein is the product of a tumor suppressor gene, p53, whose inactiv C;Comment!y: cellular tumor antigen p53 C;Kuperfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho F;164,167,227,331/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;395/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted	JH0631 C;Species: Oncorhynchus mykiss (rainbow trout) C;Accession: JH0631 R;Germentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T. Gene 112, 241-245, 1992 A;Title: Rainbow trout p53: cDNA cloning and biochemical characterization. A;Reference number: JH0631; MUID:92210006; PMID:1339362 A;Accession: JH0631 A;Molecule type: mRNA	

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R;Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P. Nucleic Acids Res. 16, 11383, 1988 A;Title: Nucleotide sequence of a cDNA encoding the chicken A;Reference number: S02193; MUID:89083584; PMID:3060861 A;Accession: S02193
                                                                                                                       N;Alternate names: nuclear oncoprotein p53
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S02193
R;Soussi, T; Begue, A.; Kress, M.; Stehelin, D.; May, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncogene 9, 109-120, 1994
A;Title: Overexpression of wild-type p53 interferes with A;Reference number: 151639; MUID:94134403; PMID:8302570 A;Accession: S61531
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    A; Residues:
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Cellular tumor antigen p53 - chicken
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A;Residues: 1-51,'S',53-70,72-293,295-363 <HOW>
A;Cross-references: EMBL:X77546; NID:g488513; PIDN:CAA54672.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-293,295-363 <HOE>
A;Residues: 1-293,295-363 <HOE>
A;Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514
R;Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, W.
submitted to the EMBL Data Library, March 1994
A;Reference number: S72313
A;Accession: S72313
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A;Title: Cloning and characterization of a
A;Reference number: A29376; MUID:88143684;
A;Accession: A29376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-363 <SOU>
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Best Local Similarity
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Keywords: apoptosis; cell division control; DNA binding; homotetramer; nu
150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                            PDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt SCAVPSTDDYAGKYGLQLDFQQNGTAKSVTCTYSPELNKLFCQLAKTCPLLVRVESPPPR}
                          mRNA
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54.5%;
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Pred. No. 2.9e-52;
42; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA from Xe
PMID:2830576
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A;Cross-references: EMBL:x81704; NID:g602332; PIDN:CAA57348.1; PID:g602333 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; ph F;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellular tumor antigen p53 - bovine W; Alternate names: tumor-suppressor protein C; Species: Bos primigenius taurus (cattle) C; Date: 10-Sep-1999 #sequence_revision 10-Se C; Accession: S51648 E; Dequiedt, F; Willems, L.; Burny, A.; Kett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741 ();Superfamily: cellular tumor antigen p53 (C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; E;161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-386 < DEQ>
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MNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTK
                                           G-LAPPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGG
                                                                                   GQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGG
                                                                                                                               PSLNKLFCQLAKTCPVQLWVDSPPPPGTRVRAMAIYKKLEHMTEVVRRCPHHERSSDYSD
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R.Soussi, T.; de Fromentel, C.C.; Breugnot, C.; May, E.

Nucleic Acids Res. 16, 11384, 1988

A; ittle: Nucleotide sequence of a cDNA encoding the rat p53 nuclea

A; Reference number: S02192; MUID:89083585; PMID:3060862

A; Accession: S02192

A; Molecule type: mRNA

A; Residues: 1-391 <SOU>
A; Cross-references: EMBL:X13058; NID:956828; PIDN:CAA31457.1; PID:

R; Hulla, J.E.; Schnelder, R.P.

Nucleic Acids Res. 21, 713-717, 1993

A; Title: Structure of the rat p53 tumor suppressor gene.

A; Reference number: $41149; MUID:93181268; PMID:8441680

A; Reference number: S41149; MUID:93181268; PMID:8441680

A; Residues: preliminary; nucleic acid sequence not shown; translatic

A; Molecule type: DNA

A; Residues: 1-173, 'W', 175-391 <HUL>

A; Cross-references: EMBL:107909

A; Note: the nucleotide sequence was submitted to the EMBL Data Lib

C; Genetics:

A; Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2

C; Superfamily: cellular tumor antigen p53

C; Keywords: apoptosis; cell division control; DNA binding; homotet

F; 174, 177, 236, 240/Binding site: zinc (Cys, His, Cys, Cys) #status

F; 390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predic
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                                                                                                                                                                                                                                                                                                    AVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEGNSHAQYVEDPIT
                                                                                                                                                                                                                                                                           TRVRAMAIYKKSQHMTEVVRRCPHHE---RCSDGDGLAPPQHLIRVEGNPYAEYLDDRQT
FTLKIRGRERFEMFRELNEALEL
                                                                                                                                 ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDEL
                                                                                                                                                                                 FRHSVVVPYEPPEVGSDYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFE
                                                                                                                                                                                                                                                                                                                                                                      --VPSQKTYQGNYGEHLGFLQSGTAKSVMCTYSISLNKLFCQLAKTCPVQLWVTSTPPPG
                                                                                                                                                                                                                                                                                                                                                                                                               PAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQG
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                                                                                     VRVCACPGRDRRTEEENFRKKEEHCPELPPGSAKRALPTST----SSSPQQKKKPLDGEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RALPTNT----SSSPQPKKKPLDGEYFTLQIRGFKRYEMFRELNDALEL-----KDALDG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 6.4e-49;
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348
                                         329
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cellular tumor antigen p53 [validated] - human %,Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppr C;Species: Homo sapiens (man) C;Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000 C;Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397; B25397; 4905; I58354; I78850; I52681; S60153 R;Lamb, P.; Crawford, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: p53
C;Superfamily: cellular tumor antigen p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho C;Keywords: apoptosis; cell division control; Cys, Cys) #status predicted F;179,182,241,245/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-396 <LES/
A; Cross-references: GB:M75144; NID:g191414;
A; Experimental source: kidney, strain MP1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Cell. Biol. 6, 1379-1385, 1986 A; Title: Characterization of the hu A; Reference number: A25224; MUID:87
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A;Cross-references: EMBL:X01405; R;Buchman, V.L.; Chumakov, P.M.;
                                      A; Molecule type: DNA
A; Residues: 1-393 <LAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 MTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 PWPLSSS--VPSYKTYQGDYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQLAKTCPVQLWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDGEYFTLKIRGQERFKMFQELNEALELKDAQALKASEDSGAHSSYLKSKKGQSASRLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRNSFEVRICACPGRDRRTEEKNFQKKGEPCPELPPKSAKRALPTNT---SSSPQPKRKT
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                                                                                              f the human p53 MUID:87064416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 712.5;
                                                                                                                                                                                                                                                                                                                                                                       393
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                                                                                              gene.
PMID:2946935
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<F01>

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A; Title: Primary structure polymorphism at amino acid residue A; Reference number: S42452; MUID:87144273; PMID:3547088 A; Accession: S42452
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-71,/p,/73-78,/T/,80-393 <HAR2>
A; Residues: 1-71,/p,/73-78,/T/,80-393 <HAR2>
A; Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell lin
R; Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford
Mol. Cell. Biol. 7, 961-963, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Molecular basis for heterogeneity of the human A;Reference number: A93086; MUID:87089826; PMID:3025664 A;Accession: A25397
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A; Moslecule type: mRNA
A; Residues: 1-71, 'p', 73-272, 'H', 274-393 <HAR>
A; Residues: 1-71, 'p', 73-272, 'H', 274-393 <HAR>
A; Cross-references: GB: K03199; NID: g189478; PIDN: AAA59989.1; PID: g189479
A; Experimental source: Clone pR4-2, cell line A431
A; Experimental source: Shohat, O; Prokocimer, M.; Wolf, D.; Arai, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-71,'p','73-393 <ZAK>
A;Residues: 1-71,'p','73-393 <ZAK-
A;Residues: 1-71,'p','73-393 <ZAK-
A;Reference number: A55060; MUID:85267676; PMID:3894933
A;Accession: A55060
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A; Residues: 101-393 < mKI1>
A; Residues: 101-393 < mKI1>
A; Cross-references: EMBL; X01405; NID: g35215; PIDN: CAA25652.1;
R; Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M.
EMBO J. 4, 1251-1255, 1985
EMBO J. 4, 1251-1255, 1985
A; Title: Human p53 cellular tumor antigen: cDNA sequence and eA; Reference number: A22837; MUID: 85230577; PMID: 4006916
A; Accession: A22837
                                  A; Experimental source: clone J6K
                                                                  A;Residues:
                                                                                                                                                                        A;Residues: 66-71,'P',73-79 <MKI2>
A;Experimental source: clone lambda Cll3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-78,'T',80-393 <HAR1>
A;Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A;Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
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A; Accession: $40773
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A;NOte: this 72-Arg allele appears to be about
A:Accession: JT0436
                                                                                         A; Molecule type: mRNA; DNA
                                                                                                                   A; Accession:
                                                                                                                                             A; Note: 72-Cys was also found,
                                                                                                                                                                                                                               A; Molecule type: mRNA; DNA
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A; Residues: 1-393 <CHU>
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     P.J.;
                                                            66-79 <MKI3>
                                                                                                                   S42453
        Allan,
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     G.J.;
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F.; Vousden,
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A;Molecule type: mRNA
A;Residues: 1-247,'Q',249-393 <F08>
A:Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-71, 'P',73-237,'Y',239-393 <F07>
A;Cross-references: EMBL:X60016; NID:g506444;
A;Accession: I38089
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A; Residues: 1-247, 'q', 249-393 <F06>
A; Cross-references: EMBL:X60015; NID:g506442;
A; Accession: I38088
A; Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-189, 'LISIASWKEICVWSIWMTETLEDIVWWCPMSRLRLALT', 'VPPSTTTTCVTVPAWAA'
A; Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
A; Note: deletion of a C nucleotide causes a frameshift at position.566
A; Accession: 138083
                                                      A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214 R;Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, Cancer Res. 51, 5800-5805, 1991
                                                                                                                                                                                                                                                                             Nucleic Acids Res. 19, 6977, 1991
A; Title: An Alu polymorphism intragenic to the TP53 gene
A; Reference number: I38093; MUID:92107726; PMID:1762941
                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453 A;Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 199 R;Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-212, 'Q', 214-393 <F10>
A; Cross-references: EMBL:X60019; NID:g506450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-71,'P',73-162,'H',164-393 <F09>
A; Cross-references: EMBL:X60018; NID:g506448;
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A; Residues: 1-245, 'T', 247-393 <F04>
A; Cross-references: EMBL: X60013; NID: g506438;
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A;Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A;Reference number: I38082; MUID:92007731; PMID:1915267
A;Accession: I38082
                            A;Title:
                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-393 <FUT>
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                                                                                                                                                                                                                                             A; Reference number: A; Accession: 138093
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A; Residues: 1-253, 'D', 255-393 <F11>
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A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-236, 'I', 238-393 <F05>
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A; Residues: 1-393 <F03>
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A; Residues: 1-192, 'R', 194-393 <F02>
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                            p53 gene mutations
3 gene mutations in gastric cancer metastases
number: A44905; MUID:92034678; PMID:1933850
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A;Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1; R;Chow, V.T.; Quek, H.H.; Tock, E.P.C. Cancer Lett. 73, 141-148, 1993
A;Title: Alternative splicing of the p53 tumor suppressor gene A;Reference number: I52681; MUID:94036762; PMID:8221626
A;Accession: I52681
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A; Molecule type: mRNA
A; Residues: 327-331, 'DQTSFQKENC' <CHO>
A; Residues: 327-631, 'DQTSFQKENC' <CHO>
A; Residues: 327-631, 'DQTSFQKENC' <CHO>
A; Note: mutant sequence with altered splicing and termination expressed in Mc
R; Petersen, G; Song, D; Huegle-Doerr, B; Oldenburg, I; Bautz, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1995
A; Title: Mapping of linear epitopes recognized by monoclonal antibodies with
A; Reference number: S60151; MUID:96133682; PMID:8552047
A; Accession: S60153
cellular tumor antigen p53 - green monkey (;Species: Cercopithecus aethiops (green rC;Date: 10-Sep-1999 #sequence_revision 10 C;Accession: S06594 R;Rigaudy, P.; Eckhart, W.
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J. Biol. Chem. 264, 18019-18023, 1989
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A;Cross-references: GB:S63157; NID:g237829; PIDN:AAB20140.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:63157, 1
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A; Residues: 3-44 <PET>
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;Residues: 244-247,'W',249-252
;Cross-references: GB:S41969; N
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Residues: 246-2
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Pred. No. 6.8e-48;
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A; Molecule type: mRNA
A; Residues: 1-393 < RIG>
A; Residues: references: EMBL: X16384; NID: g22795; PIDN: CAA34420.1; PID: g22796
A; Cross-references: EMBL: X16384; NID: g22795; PIDN: CAA34420.1; PID: g22796
A; Cross-references: EMBL: X16384; NID: g22795; PIDN: CAA34420.1; PID: g22796
                                                                                                                                                                   A;Reference number: A02684; MUID:84068204; PMID:6646235
A;Accession: A02684
A;Molocolo ****
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C;Date: 28-Aug-1955 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C;Accession: A22739; 505336; A02684; S38822; S38823; S40014; I48703
R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nuc;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nuc;Keywords: apoptosis; cell division covers.
E;176,179,238,242/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
E;392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                               A; Molecule type: mRNA
A; Residues: 1-159, 'H',161-167, 'G',169-233, 'I',235-390 <ZAK>
A; Residues: 1-159, 'H',161-167, 'G',169-233, 'I',235-390 <ZAK>
A; Cross-references: GB:X01237; GB:K01700; NID:953575
A; Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Sh
Mol. Cell Biol. 6, 3232-3239, 1986
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DNMS53
cellular tumor antigen p53 - mc
cellular tumor antigen p53 - mc
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A; Reference number: S06594; M
                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-134,'V',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-134,'V',136-390 .
A; Cross-references: GB:X00876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 3, 2179-2183, 1984
A;Title: Analysis of the gene coding for the murine cellular A;Reference number: A22739; MUID:85027173; PMID:6092064
A;Accession: A22739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Bienz, B.; Zakut-Houri,
EMBO J. 3, 2179-2183, 198
A; Title: Immunologically distinct A; Reference number: S38822; MUID:8
                                                                                                                                                                                                                                                                                                                                                                          A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S06336
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Primary structure of DNA complementary to murine A; Reference number: S06336; MUID:88221682; PMID:3329909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bioorg. Khim. 13, 1691-1694, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Chumakov, P.M.
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                                                                                                                                                                                                                                                                                                                  1-134,'V',136-390 <CHU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRP
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                                                                                                                                                                                                                                                                                               R.; Oren,
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MUID:87064640; PMID:3023970
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; NID:g871420; PIDN:CAA25420.1;
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Pred. No. 1.4e-47;
1; Mismatches 82;
                                                                                                                                                                                                                                                                                            B.,
                                                                                                                                                                                                                                                                                            Lavie, V.; Hazum,
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F;114-139/Region: conserved region II
F;160-192/Region: L2 loop
F;168-178/Region: conserved region III
F;231-252/Region: conserved region IV
F;231-252/Region: conserved region V
F;233-248/Region: L3 loop
F;267-283/Region: nuclear location signal
F;313-319/Region: nuclear association
F;319-357/Region: tetramer association
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A; Residues: 1-167,'G',169-233,'I',235-390 <ARA2>
A; Cross references: EMBL:M13873
R; Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill,
submitted to the EMBL Data Library, July 1988
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-167,'G', 169-390 <ARA3>
A; Residues: 1-167,'G', 169-390 <ARA3>
A; Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1;
A; Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA3982.1;
A; Cross-references: EMBL:M13873; NID:g200200; NID:g
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A;Title: Cloning and expression analysis of full length mouse A;Reference number: I48703; MUID:84272240; PMID:6379601
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A; Accession: S40014
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A; Residues: 1-390 <ARA1>
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146; Conserv
                                                                                                                                          LPPGSAKRALPTCT---SASPPQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---
AHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVK 383
                                                                                                                                                                                                                                                                                                                              KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
                                                                                                                                                                                                                                                                                            NSSCMGGMNRRPILTITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEVLCPE
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                                                             TYROQQQQQHQHLLQK 355
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Conservative

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32;

Gaps

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A;Gene: p53
C;Superfamil
C;Keywords:
                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-393 <LEE>
A;Cross-references: GB:U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230
C;Comment: This protein is a multimer, it plays the central role in a compliption, and recombination by protein/protein interactions.
C;Genetics:
                                                                                                                                                                                                                                                                              K;Lee, H.; Larner, J.M.; Hamlin, J.L.
Gene 184, 177-183, 1997
A;Title: Cloning and characterization of Chinese hamster
A;Reference number: JC6176; MUID:97183659; PMID:9031625
A;Contents: liver
                                                                                                                                                                                                                                                                                                                                                                                                      tumor suppressor protein p53 - Chinese C; Species: Cricetulus griseus (Chinese C; Date: 11-Apr-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: p53
C;Superfamily: cellular
C;Keywords: tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumor suppressor p53 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997
C;Accession: JC6193
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A; Residues: 1-391 <LEA>
A; Cross-references: EMBL:X90592; NID:g1532043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: cDNA cloning and immunological characterization A;Reference number: JC6193; MUID:97208869; PMID:9055811 A;Accession: JC6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Le Goas, F.; May, P.; Ronco, P.; de Fromentel, C.C. Gene 185, 169-173, 1997
                                                                                                                                                                                                                                                               A; Accession: JC6176
                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: JC6176
                                                                                                    Superfamily:
  Matches 151;
                                       Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 DSSPQTKKKPLDGEYFILKIRGRERFEMFRELNEALEL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 RVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TFDAL-SPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQI
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                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENNAQTQFSEPQYTNL----GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKTCPVQLWVDSTPPPGTRVRAMAIYKKSQHMTEVVRRCPHHE--RCSDSDGLAPPQHLI
                                                                                                    cellular tumor antigen p53
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                    33.5%;
42.7%;
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Score 698; DB 2;
Pred. No. 3.5e-47;
0; Mismatches 111
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Pred. No. 2.4e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                          hamster
hamster)
09-May-1997 #text_change 23-Jul-1999
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                                       Length 393;
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Mol. Cell. Boll. 6, 322-323, 1986

A:Title: Immunologically distinct p53 molecules generated by alternative splicing.

A:Reference number: $38822; MUID:87064640; PMID:3023970

A:Accession: $38824

A;Molecule type: mRNA

A;Residues: 1-381 <ARA>

A;Cross:references: GB:M13874; NID:9200202; PIDN:AAA39883.1; PID:9200203

R;Han, K.A.; Kulesz-Martin, M.F.

Nucleic Acids Res. 20, 1979-1981, 1992

A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different tis A;Reference number: $35478; MUID:92253421; PMID:1579500

A;Accession: $35478; MUID:92253421; PMID:1579500

A;Accession: $35478; MUID:92253421; PMID:1579500

A;Accession: S36478; MUID:92253421; PMID:1579500

A;Cross:references: EMBL.M13874; NID:9200202; PIDN:AAA39883.1; PID:9200203

A;Note the nucleotide sequence was submitted to the EMBL Data Library, July 1988

C;Comment: This sequence, produced by alternative splicing of the tenth intron, lacks to not known.

C;Superfamily: cellular tumor antigen p53

C;Keywords: alternative splicing; phosphoprotein; zinc

F;16-26/Region: conserved region II

F;160-192/Region: DNA-binding core #status predicted <DBC>

F;104-139/Region: conserved region II

F;161-18/Region: conserved region II

F;162-18/Region: conserved region II

F;263-28/Region: conserved region II

F;267-28/Region: conserved region IV

F;267-28/Region: conserved region IV

F;267-28/Region: conserved region IV

F;267-28/Region: conserved region IV

F;267-28/Region: conserved region IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
$38824
$38824
cellular tumor antigen p53, minor splice form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: $38824; $35478
R;Arai, N; Nomura, D; Yokota, K; Wolf, D; Brill, E; Shohat,
Mol. Cell. Biol. 6, 3232-3239, 1986
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                                                                                                     F;267-283/Region: conserved region V
F;313-319/Region: nuclear location signal
F;313-319/Region: tetramer association
F;319-357/Region: tetramer association
F;7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
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Best Local Similarity
Matches 139; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LELMQYLPQHTIE-----TYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKGEPCPELPPKSAKRALPTNT---SSSPPPKKKTLDGEYFTLKIRGHERFKMFQELNEA
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                Conservative
                                  33.0%;
                49;
          Score 687; DB Pred. No. 2.4e
          DB 2; I
2.4e-46;
hes 81;
                                                          Length 381;
             Indels
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             26;
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hypothetical protein K10G6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: C2enorhabditis elegans
C;Access: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-
C;Accession: T32008
R;Davidson, S.; Wohldmann, P.; Mullen, G.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid K10G6.
A;Reference number: Z21111
A;Accession: T32008
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1819 <DAV>
A;Cross-references: EMBL:AF016669; PIDN:AAB66098.1; GSPDB:GN00020; CESI
A;Experimental source: strain Bristol N2; clone K10G6
C;Genetics:
A;Gene: CESP:K10G6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, Anticancer Res. 14, 2039-2046, 1994
A;Title: The canine p53 gene is subject to somatic mutations in thypoid carcinoma.
A;Reference number: I46226; MUID:95150524; PMID:7847847
A;Accession: I46226
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-77 CDEV>
A;Cross-references: GB:L27630; NID:9508454; PIDN:AAC37327.1; PID:9508455
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellular tumor antigen p53 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1997 #sequence_revision 21-F
C;Accession: I46226
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C; Superfam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 LPPGSAKRALPTCT---SASPPQKKKPLDGEYFTLKIRGRKRFEMFRELNEALEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24/1; 61/3
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No. 1.1e-13;
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                                                                                        CESP:K10G6.3
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 9F1
A;Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
A;Note: bassoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T42730
R;Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A;Reference number: Z22249; MUID:98345363; PMID:9679147
A;Accession: T42730
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3942 < DIE>
A;Cross-references: EMBL:X17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
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A; Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bassoon protein – mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863 IQFQQQQQRFQHHQQQQQAGRIPPRPPNPILNQVQNPPQQVQHNQHQNQMLNPI--RQP 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        803 TYTKTTVPPSVANTWNTEKAQLISPKPRSQTIFSEASSSMTVGDALRAQQHQQKMDQQIQ 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           749 KVAASSSSNSAASRPPSQPSTPATAPATPMLQASQAPQPLQAPPQSPMET-----TATV 802
                                                                                                                                           23 LNSMDQQ-IQNGSSSTSP----YNTDHAQNSVTAPSPYAQPSS-----TFDALSPSPAI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 QIQNGSSSTSPYNTDHAQNS--VTAP-SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDV 85
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Similarity 19.4%;
PGNLAQYGPAASQATAVRQLLPSTATVRAADGMIYST----INTPIAATLPITTQPASVL 222:
                                  PSNTDYPGPHSFDVSFQQSSTAKSAT-----WTYSTELKKLYCQIAKTCPIQIK---VM 122
                                                                                            LNSMDQYGGRHGSGSGGPDLVQYQPQHGP-GLSAPQGLAPLRSGLLGNPTYPEGQPS--- 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HQHLLQKHLLSACFRNELVEPRRETPKQSDV 379
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                                                                                                                                                                                             Conservative
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ce: strain 129 SVJ
                                                                                                                                                                                        5.2%; Score 109; DE 21.6%; Pred. No. 16; tive 57; Mismatches
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Pred. No. 3.6;
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QQLQLQLEEQKQRQKAPFP 2486
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                              KOSDVFFRHSKPPNRSVYP
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                                                                                                                                              KQQE-----
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Search completed: August 7, 2003, 09:53:31
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Result
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Kaelin W.G. Jr.;
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Kharbanda S., Weichselbau
Nature 400:792-792(1999).
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Kharbanda S., Weichselbaum R., Kufe D.;
"p73 is regulated by tyrosine kinase c-Abl in
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[8]
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DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN NEUROBLASTOMA AND OLICODENDROGLIOMA.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                     ISOId=015350-7; Sequence=VSP_006538; TISOID=01550-7; Sequence=VSP_006538; TISOID=SPLEIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEA SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS. INDUCTION: NOT INDUCED BY DNA DAMAGE.
DOMAIN: POSSESS AN ACIDIC TRANSACTIVATION DOMAIN, A CE BINDING DOMAIN AND A C-TERMINAL OLICOMERIZATION DOMAIN AND TO THE ABL TYROSINE KINASE SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE TYPOSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPIC AND WITH P53, WHEREAS ISOFORM ALPHA DOSE NOT. ISOFORM GAMMA INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DINTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
                                                                                                                                                                                                                                        Name=Kappa;
IsoId=015350-7;
                                                                                                                                                                                                                                                                                                                                                                                        Name=Epsilon;
IsoId=O15350-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                     IsoId=015350-5; Sequence=VSP_006544, Note=The splicing of exon 11 results original reading frame. The splicing reading frame to the sequence of isof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note=The splicing of ex original reading frame;
                                                                                                                                                                                                                                                                                IsoId=015350-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=015350-3; Sequence=VSP_006540,
Note=The splicing of exon 11 results
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=015350-2;
                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=015350-4; Sequence=VSP_006542,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=015350-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAY-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shioya H., Ishiko T., Sun X., Weichselbaum R., Kufe D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p53 gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: Nuclear.
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                                                                                                                                                                                                                                                                             Sequence=VSP_006546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence=VSP_006539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                        the sequence of isoform Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAPPA)
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                                                                                                                                                                                                                                                                                                                                           VSP_006545;
in a frameshift
of exon 13 rever
                                                                                                                                                                                                                                                                                                                                                                                                                             VSP_006543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSP_006541;
in a frameshift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang Y., Lu H.,
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PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation;
Apoptosis; Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0003700; F:transcription factor activity; TAS. GO; GO:0008630; P:induction of apoptosis by DNA damage; GO; GO:0006298; P:mismatch repair; TAS. InterPro; IPR002117; P53.
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                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 601990;
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                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                    DOMAIN
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.ew; HGNC:12003; TP73.
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Y11416; CAA72221.1
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CAB92742.
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n; Phosphorylation; Alternative splicin
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             isoform Kappa).
/FIId=VSP_006538.
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SELTGLECPNOLIEYFTSOGLQSIYHLQNLTIEDLGALKIPE
QYRMTIWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGE
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POLY-PRO.
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DCKARKQPIKEEFTEAEIH
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ID P73_C
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C ELWART
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935K8; 99TS99;

16-CCT-2001 (Rel. 4

16-CCT-2001 (Rel. 4

28-FEB-2003 (Rel. 4

Tumor protein p73 (
                                      between
the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithe
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TP73 OR P73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                  ISOId-Q9XSK8-2; Sequence-VSP_006537;
DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAI BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION TO THE ABL TYROSINE KINASE SH3 DOMAIN.
SIMILARITY: BELONGS TO THE P53 FAMILY.
      European
by non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND WITH P53, WHEREAS ISOFORM SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS
TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                      Event-Alternative Name-Alpha;
                                                                                                                                                                                                                                                                                                                                           Name=Beta;
                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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P53_ONCMY

P55035;

O1-MAY-1992 (Re.)

O1-MAY-1992 (Re.)

Cellular tumor a
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ProDom; PD002681; P55; 1.
SMART; SM00454; SAM; 1.
PROSITE: P500348; P53; 1.
Transcription regulation; Active Apoptosis; Nuclear protein; Phosynarsplic 495 637 SF;
                                                                                                         Oncorhynchus mykiss (Rainbow trout) (Sa
Dukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Protacanthopterygii; Salmoniformes; Sal
SEQUENCE FROM N.A.
MEDLINE-92210006; PubMed-1339362;
de Fromentel C.C., Padkel F., Cha
"Rainbow trout p53: cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y11419; CAA72224.1;
EMBL; Y11419; CAA72225.1;
HSSP; O15350; 1COK.
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                                                                                          NCBI_TaxID=8022;
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n; Phosphorylation; Alternative splicing.
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QYRMTIMRGLQDLKQGHDYGAAAQQLLRSSNAAAISIGGSG
ELQRQRVMEAVHFRVRHTITIPNRGGPGAGPDEWADRGFDL
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annotation updat
                                                                                                             Teleostei; Euteleostei; formes; Salmonidae; Onco
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1.4e-87;
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RESULT 4
P53_BARBU
ID P53_B,
AC Q9W67
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Best Local S
Matches 169
P53_BARBU
Q9W678;
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ProDom; PD002681; P53; 1.
PROSTTE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on if
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JH0631; JH0631.
HSSP; P04637; ITUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M75145; AAA49605.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Phosphorylation; Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                         339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                   FRQ-NTHGIQMTSIKKRRS----PDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI
                                                                                                                                                                                                                                                                                                                                                                                                                           HECQLAKTCPVQIVVDHPPPPGAVVRALAIYKKLSDVADVVRCPHHQSTSENNEGP-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTAPSPYAQPS-STFDALS-PSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKK
                                                                                                                  DKYRQK 365
                                                                                                                                                         ETYRQQ 344
                                                                                                                                                                                                MKEASLPAPQPGASKKTKSSPAVSDDEIYTLQIRGKEKYEMLKKFNDSLELSELVPVADA
                                                                                                                                                                                                                                                                          ILTITLETQEGQLLGRRSFEVRVCACPGRDRKTEEINLKKQQETTLETKTKPAQGIKRA
                                                                                                                                                                                                                                                                                                              ILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQ---VSDSTKNGDGTKRP
                                                                                                                                                                                                                                                                                                                                                       RGHLVRVEGNQRSEYMEDGNTLRHSVLVPYEPPQVGSECTTVLYNFMCNSSCMGGMNRRP
                                                                                                                                                                                                                                                                                                                                                                            PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSATEPAPQPSISTLDTGSPPTSTVPTTSDYPGALGFQLRFLQSSTAKSVTCTYSPDLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303
395
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                  STANDARD;
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356
392
318
395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
PHOSPHORYLATION (BY SIMILARITY).
8422250765545A1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 839.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTION ACTIVATION (ACIDIC) BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OLIGOMERIZATION.
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                  369
                  A
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MBL outstation -
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Best Local S
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MOD_RES
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                                                                                                                                   148
                                                                                                                                                                         78
                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                            29
                  VLYNFMCNSSCMGGMNRRPILTIISLETHDGQLLGRRSFEVRVCACPGRDRKTEESNFRK
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Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).

DNA_BIND 66 256 BY SIMILARITY.

DOMAIN 298 329 OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barbus barbus (Barbel).
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Barbus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, I
28-FEB-2003 (Rel. 41, I
Cellular tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF071570; AAD34212.1; HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00386; P53SUPPRESSR.
                                                                                                                                                                                                              QQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPYYKKAEHVTEVV
                                                                                                                                                                                                                                                                              ELINDEYLPSSFDPNIFDNVLTEQPQPSTSP-----PTASVPVATDYPGEHGFKLGF
VLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRK
                                                                                                                       KRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTT
                                                                                                                                                                                                                                                                                                                                   QIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSF
                                                                       RRCPHHERTPD-GDG-LAPAAHLIRVEGNSRALYREDDVNSRHSVVVPYEVPQLGSEFTT
                                                                                                                                                                              PQSGTAKSVTCTYSSDLNKLFCQLAKTCPVQMVVNVAPPQGSVIRATAIYKKSEHVAEVV
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298
342
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40, Last sequence update)
41, Last annotation update)
tigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355
365
368
                                                                                                                                                                                                                                                                                                                                                                                                        39.4%;
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Pred. No. 2.
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NUCLEAR LOCALIZATION SIGNAL (POTE
PHOSPHORYLATION (BY SIMILARITY).
OBEZCFZCEA74C304 CRC64;
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Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                . 8e-55
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            DNA_BIND
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                                                                                                                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; El
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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01-NOV-1997 (Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyprinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellular tumor antigen p53
                                                                        DOMAIN
                                                                                    Nuclear protein; Phosphorylation;
                                                                                                   Anti-oncogene;
                                                                                                              ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                              PRINTS; PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                          expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRARE
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BAX and FAS antigen
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P04637;
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 70
301
345
280
372
                                                                                                DNA-binding; Transcription
                                                                                                                                                                                                                  AAB40617.1;
AAA97408.1;
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   360
366
396
372
                                                                                                                                                                                                                                                                                                                                                                                                                                      expression, or by repression of Bcl-2
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            BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE
                                          OLIGOMERIZATION
                                                      TRANSCRIPTION ACTIVATION
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                     There are no rest
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                                                                                                regulation;
                                                                                                                                                                                                                                                                                        Usage
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SIMILARITY)
                                                                                                                                                                                                                                                                                         ЬY
                                                                                                Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cypriniformes;
                                                                    (ACIDIC)
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            (POTENTIAL).
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P53_ICTP 6
P53_ICTP
ID P53_ICTP
ID P53_ICTP
ID 16-OC
DT 16-OC
DT 16-OC
DT 28-FE
DE CALL
GN TP53
OS ICTAL
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CC ICTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P53_ICTPU
093379;
                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-99071979; PubMed-9854815;

Luft J.C., Bengten E., Clem L.W., Miller N.W.,

Luft J.C., Bengten E., Clem L.W., Miller N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ictalurus punctatus (Channel c
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   channel catfish (Ictalurus punctatus).";
Comp. Biochem. Physiol. 120B:675-682(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cellular tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7998
                                                                                                                                                                    BAX and FAS antigen expression, or by expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          the tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ostariophysi;
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DT 28-F
DT 28-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P53_XENLA
P07193;
SEQUENCE.FROM N.A.
MEDLINE-94134403; PubMed-8302570;
Hoever M., Clement J.H., Wedlich |
"Overexpression of wild-type p53
in Xenopus laevis embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1988 (Rel. 07,
01-APR-1988 (Rel. 07,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
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ProDom; PD002681; P53; 1.

PROSITE; P500348; P53; 1.

Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Me
                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                      Cellular
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                                                                                                                                                       for a
                                                                                                                                                                                                                      MEDLINE=88143684; PubMed=2830576;
                                                                                                                                                                                                                                                                                                              Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                i T., de Fromentel C.C., Mechali M., May
ing and characterization of a cDNA from
protein homologous to human and murine
ene 1:71-78(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA 112
                                                                                                                                                                                                                                          FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LLSKTCRKERDGAAGEPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQKHLLSACFRNE----LVEPRR 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASKKSKNSSSDDEIYTLQVRGKERYEFLKKINDGLELSDVVPPADQEKYRQK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LETQDGHLLGRRTFEVRVCACPGRDRKTEESNFKKQQ~EPKTSGKTLTKRSMKDPPSHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002117; P53.
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347
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375
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                                                                                                                                                                                                                                                                                                       Xenopus
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                   p53
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                                                                                                                                                                                                                                                                                                                                                                                                                 (Tumor suppressor
                                                                                                                                                                                                                                                                                                                           a; Craniata; Vertebrata;
Mesobatrachia; Pipoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 800; DB 1; Pred. No. 8.9e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSCRIPTION ACTIVATION (ACIDIC) BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY SIMILARITY).
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1B89CD98DB3289F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                               D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362
                        interferes
                      Montenarh M., Knoechel W.; erferes with normal develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ⋛
                                                                                                                                                                                               Мау Р.,
                                                                                                                                                                                                                                                                                                                              Pipoidea;
                                                                                                                                                    Xenopus p53.";
                                                                                                                                                                                                                                                                                                                                                                                                                 p53).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 376;
                      normal development
                                                                                                                                                                                               Kress M.;
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                                                                                                                                                                           laevis
                                                                                                                                                                                                                                                                                                                              Pipidae;
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Matches 151
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CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M36962; AAA49923.1; -.
EMBL; X05191; CAA28821.1; -.
EMBL; X77546; CAA54672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S68353; AAC60746.1;
PIR; A29376; A29376.
HSSP; P04637; LTUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBUNIT: Binds DNA as a homotetramer (
-i- SUBCELLULAR LOCATION: Nuclear.
-i- TISSUE SPECIFICITY: Ubiquitous.
-i- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncogene 9:109-120(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                 Local Sin hes 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 suppression (By similarity).

SUBDINIT: Binds DNA as a homotetramer (By similarity).

SUBCELLULAR LOCATION: Nuclear.
                                                                                                              187
                                                                                                                                          188
                           302
                                                      247
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                                                                                                                                                                                                                            68
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                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR00386; P53SUPPRESSR.
                                                                                                                        GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFE 247
                                                                                                                                                                                  GAVIRAMPYYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT 187
DDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV
                                                      VRVCACPGRDRRTEEDNYTKKRGLKPSGK
                                                                                                                                                                                                                                           SPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
                         PDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI
                                                                               ARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKRR----S
                                                                                                              GRHSVCVPYEGPQVGTECTTVLYNYMCNSSCMGGMNRRPILTIITLETPQGLLLGRRCFE
                                                                                                                                                                      GSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYMEDVNS
                                                                                                                                                                                                                           SCAVPSTDDYAGKYGLQLDFQQNGTAKSVTCTYSPELNKLFCQLAKTCPLLVRVESPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit
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281
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71
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                           AĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation; Apoptosis.
29 TRANSCRIPTION ACTIVATION
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                        267
331
356
293
362
52
71
                                                                                                                                                                                                                                                                                                                                           40692 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rmatics Institute. There are no rest institutions as long as its content
                                                                                                                                                                                                                                                                                                36.6%;
54.5%;
                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is not removed.
                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY SIMILARITY).
7 -> S (IN REF. 2).
MISSING (IN REF. 2).
MISSING (IN REF. 2).; CE1F3E58F020D74D CRC64;
                                                                                                                                                                                                                                                                                 Score 762; DB 1;
Pred. No. 6.7e-51
2; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                               BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.isb-sib.
                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                           338
                                                                                                                                                                                                                                                                                                            Length 363;
                                                      RELAHPPSSEPPLPKKRLVVVD
                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Activator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is
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Best Local
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-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 16:11383-11383(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Archosauria; Aves; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002117; p53. Pfam; pF00870; p53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-SPAFAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P53_CHICK
                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S02193; S02193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of a cDNA encoding the oncoprotein ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003
                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                         DNA_BIND
                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                       Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                         Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X13057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89083584; PubMed=3060861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                            _RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                    119
                                                                  108
                                                                                                                                                                                                                                                                                                                                                                                                                                                  P04637; 1TUP
    168
                                                                                                 61
                                                                                                                               48
                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and this statement is not removed. requires a license agreement (See
                                                    YCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPP
                                                                                                                           SVTAPSPYAQPSSTEDALSPSPAIPSNTDYPGPHSEDVSFQQSSTAKSATWTYSTELKKL 107
 SHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPI 227
                                 YCRLAKPCPVQVRVGVAPPPGSSLRAVAVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPA
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292
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                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAA31456.1;
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                                                                                                                                                                                                                                                                                                                                     Phosphorylation;
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41, Last
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366
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Neognathae; Galliformes; Phasiani
                                                                                                                                                                                                                           40169
                                                                                                                                                                          36.4%;
                                                                                              -TPPRAAPSPVVPSTEDYGGDFDFRVGFVEAGTAKSVTCTYSPVLNKV 118
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                                                                                                                                                                                                                                                                                                                                                    Transcription regulation;
                                                                                                                                                                           Score 758.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                       TRANSCRIPTION ACTIVATION BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                                                                                        NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                      BASIC (REPRESSION OF DNA-BINDING)
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                                                                                                                                                           Mismatches
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Phasianidae; Phasianinae;
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PS3_PIG 10 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9TUB2;
16-OCT-2001
                                                                                              DOMAIN
                                                                                                           Nuclear
                                                                                                                                          PROSITE;
                                                                                                                                                                                            Pfam; PF00870; P53;
                                                                                                                                                                                                         InterPro; IPR002117;
                                                                                                                                                                                                                          HSSP; P04637; 1C26
                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003
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                                                                                                           protein;
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or send an email to license@isb-sib.ch).
                                                                                                                                                           Anti-oncogene; DNA-binding;
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ISDLINE-99422034; PubMed-10490836;

Surr P.D., Argyle D.J., Reid S.W.J., Nasir L.;

"Nucleotide sequence of the porcine p53 cDNA, and "Nucleotide sequence n53 expressed in vitro with a
                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
ities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Acts as a tumor suppressor in many tumor types; induce growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation cell and fas antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Binds DNA as a homotetramer (By similarity). SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: p53 is found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                       AF098067; AAF04620.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transformed cells.
                                                                                                                                                                              PD002681; P53; PS00348; P53;
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                                                                                       Phosphorylation; Apoptosis.
45 TRANSCRIPTION ACTIVATION
285 BY SIMILARITY.
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                                                                                                                                                         Transcription regulation;
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  NUCLEAR LOCALIZATION PHOSPHORYLATION (BY P
                                                                  OLIGOMERIZATION
                                               BASIC
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AR LOCALIZATION SIGNAL (POTE
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iety of anti-p53
MAL (POTENTIAL).
                                                                                                              (ACIDIC)
                                                                                                                                                              Activator
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Best Local
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P41685;
01-NOV-1995 (Rel. 32, Cr
01-NOV-1995 (Rel. 32, La
28-FEB-2003 (Rel. 41, La
Cellular tumor antigen p
TP53 OR TRP53.
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SEQUENCE
                                                                                                                                                                                                                                                                                 MEDLINE=94333960; PubMed=8056458;
Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y.,
Watari T., Goitsuka R., Tsujimoto H., Hasegawa A.;
"Cloning of feline p53 tumor-suppressor gene and it
                                                                                                                                                                                                                                                                                                                                                                                             Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
NCBI_TaxID=9685;
                                                                                                              "Molecular cloning and chromosomal mapping suppressor gene.";
J. Vet. Med. Sci. 55:801-805(1993).
                                                                                                                                                                  O'Brien S.J.,
                                                                                                                                                                                Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T.,
                                                                                                                                                                                               SEQUENCE OF 34-354 FROM N.A. MEDLINE-94114699; Pubmed-8286534;
                                                                                                                                                                                                                                                                     hematopoietic
                                                                                                                                                                                                                                                                                                                                                    TISSUE=Lymph
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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             FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Input of cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.
   Apoptosis
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                                                                                                                                                                                                                                                                                                                                                    node;
                                                                                                                                                                  Tsujimoto H., Hasegawa A.;
   induction
                                                                                                                                                                                                                                                                     tumors."
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                                                                                                                                                                                                                                                   58:602-607(1994).
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43.0%;
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en p53
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   seems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 757.5;
Pred. No. 1.6
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   to be mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                    Futeleostomi;
                                                                                                                                                 p53
                                                                                                                                                                                   Goitsuka
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                                                                                                                              RESULT 11
P53_BOVIN
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Best Local S
Matches 147
                                           P53_BOVIN STANDARD;
Q29678;
Q19678;
Q1-NOV-1997 (Rel. 35, Create
Q1-NOV-1997 (Rel. 35, Last s
28_FEB-2003 (Rel. 41, Last a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
CONFLICT
SEQUENCE
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EMBL; D16460; 1
HSSP; P04637;
               Cellular tumor antigen p53 TP53.
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-oncogene; DNA-binding; Trans
Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
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taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear. DISEASE: p53 is found in incre of transformed cells. p53 is f
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147; Conser
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285
386
(Bovine),
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318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
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                                                                                                                                                                                                                                       PPPGSTKRALPPST---SSTPPQKKKPLDGEYFTLQIRGRERFEMFRELNEALEL
                                                                                                                                                                                                                                                                                KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLEL
                                                                                                                                                                                                                                                                                                                                                          NSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDST
                                                                                                                                                                                                                                                                                                                                                                                                                              RCPDSSDG-LAPPQHLIRVEGNLHAKYLDDRNTFRHSVVVPYEPPEVGSDCTTIHYNFMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYTCTYSPPLNKLFCQLAKTCPVQLWVRSPPPPGTCVRAMAIYKKSEFMTEVVRRCPHHE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHAQNSVTAPSPYAQPSSTFDALSPSPAI-----PSNTDYPGPHSFDVSFQQSSTAK 94
                                                                                                                                                                                                                                                                                                                                    NSSCMGGMNRRPIITIITLEDSNGKLLGRNSFEVRVCACPGRDRRTEEENFRKKGEPCPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDASGMSAVPAPAAPAPAT-----PAPAISWPLSSFVPSQKTYPGAYGFHLGFLQSGTAK 112
Created)
Last sequence update)
Last annotation update)
n p53 (Tumor suppressor p53).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 753.5;
Pred. No. 3.7
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TRANSCRIPTION ACTIVATION (ACIDIC)
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLIGOMERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frequently
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Query Match
Best Local Similarity
                                                         MOD_RES
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.; "Predominant p53 mutations in enzootic bovine leukemic cell lines."; yet. Immunol. Immunopathol. 52:53-63(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dequiedt F., Kettmann R., Burny A., Willems L.; "Nucleotide sequence of the bovine P53 tumor-suppressor cDNA."; DNA Seq. 5:261-264(1995).
                                                                                                                                                                                                                   PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                   EMBL; X81704; CAA57348.1; -. EMBL; D49825; BAA08629.1; -.
                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bishop R.R.P., Gobright E.E.I.; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                           SEQUENCE
                                                                                                                  DOMAIN
                                                                                                                                               DOMAIN
                                                                                                                                                           DNA_BIND
                                                                                                                                                                                                        Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-B.indicus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Bovine; STRAIN-Holstein; MEDLINE-96401400; PubMed-8807776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 13-386 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95352829; PubMed-7626789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-Bovine; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria
Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos indicus (Zebu).
                                                                                                   MOD_RES
                                                                                                                                 DOMAIN
                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                               [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression.

- SUBCULIVAR LOCATION: N

- DISEASE: p53 is found i

of transformed cells, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes regulared for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE P53 FAMILY
                                                                                                                                                                                                                                                                                         ; U74486; AAB51214.1;
S51648; S51648.
; P04637; ITUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in many types of cancer
                                                                                                                                                                                                                                                             PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     many types is journed in increased amounts in a transformed cells, p53 is frequently mutated
                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                                                                           IPR002117; P53.
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                                        380
386
                                                                                                   94
318
361
304
                                                                                                                                                                                                 DNA-binding; Transcription regulation; Activator;
                                           ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9915;
                                                                                                                                                                                         Phosphorylation;
                                                                                                   285
285
349
380
316
15
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                                                         380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
                                           43255
35.8%;
41.7%;
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Score
Pred.
                                                         ×
                                                                                                BASIC (REPRESSION OF NUCLEAR LOCALIZATION PHOSPHORYLATION (BY I
                                                                   PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                               OLIGOMERIZATION
                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                         ion; Apoptosis.
TRANSCRIPTION ACTIVATION
                                           222473F28C548F31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Thymus
                                                         T (IN REF.
745.5; DB 1
No. 1.3e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                       as its content
            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity)
                                                                                                                                                                                                                                                                                                                                                                                                          Usage
                                           CRC64;
                                                                                                   PRPK)
                                                                                                                  SIGNAL (POTE
            Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          wide variety or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                          ş
                                                                                                                                                                         (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovoidea;
                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                          tor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TETMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P53_TETMU
Q9W679;
            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                      Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.; "Evolutionary conservancy of p53 gene sequences in fish. Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii; Neopterygii; Teleostei; Eu
Acanthomorpha; Acanthopterygii; Percomorph
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellular tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=94908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon miurus (Congo puffer)
                                                                                                                                                              expression (By similarity).
SUBUNIT: Binds DNA as a hom
SUBCELLULAR LOCATION: Nucle
                                                                                                                                                                                                                                    FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                  SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                  BAX and FAS antigen expression, or by repression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 PSLNKLFCQLAKTCPVQLWVDSPPPPGTRVRAMAIYKKLEHMTEVVRRCPHHERSSDYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPGESRAHSSHLKSKKRPSPSCHKKPML - - KREGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRQQQQQQH-QHLLQKHLLS-ACFRNELVEPRRETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPFRQNTHGIQMTSIKKRRSP-DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-LAPPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPSAPAAPPPAT----PAPATSWPLSSFVPSQKTYPGNYGFRLGFLQSGTAKSVTCTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SPYAQPSSTFDALSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RALPTNT----SSSPQPKKKPLDGEYFTLQIRGFKRYEMFRELNDALEL-----KDALDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNRRPILTITLEDSCGNLLGRNSFEVRVCACPGRDRRTEEENLRKKGQSCPEPPPRSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELNVEPPLSQETFSDLWNLLPENNLLSSELSAPVDDLLPYTDVATWLDECPNE--APQMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENNAQTQFSEPQYTNLGLL----NSMDQQIQNGSSSTSPYN-----TDHAQNSVTAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Created)
(Rel. 40, Last sequence up
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53 (Tumor suppressor
                                                                                                                                                                    Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                                                                                                                    homotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                   P53 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367
                                                                                                                                                                                                                                                                                                                                                                         sequences in fish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostom1;
Euteleoste1; Neoteleoste1
rpha; Tetraodont1formes;
                                                                                                                                                                                  (Ву
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                              as
                            http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119;
                                            Usage
                                                                                                                                                                                    similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374
                                                              its content
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                                              ру
                                                                                                                                                                                                                    O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neoteleostei;
                                                                                restrictions
                                                and
                                                                                                EMBL
                                                                                                                                                                                                                     Bc1-2
                                                                 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                   a collaborationMBL outstation
                                                ior
                                                                                                outstation
                                                                 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                 o
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P53_CANFA
ID P53_CANFA
ID P53_CANFA
ID P53_CANFA
AC 0.2953
DT 01-NC
DT 15-DB
DT 28-FE
DE CELLU
GN TP53]
OS CANIS
OC EUKAA
OC MAMMARA
OC MAMMARA
OX NCBL,
RN [1]
RP SEQUI
RA Veldi
RT 11SO
RT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P53_CANFA STANDAND,

Q29537; Q9TV78;

Q1-NOV-1997 (Rel. 35, Created)

15-DEC-1998 (Rel. 37, Last sequence update).

28-FEB-2003 (Rel. 41, Last annotation update)

28-FEB-2003 (Rel. 41, Last annotation update).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein; Phosphorylation; DOMAIN 1 47 TRANS DNA_BIND 86 273 BY SI DOMAIN 308 337 OLICO DOMAIN 342 363 BASIC DOMAIN 342 363 BASIC DOMAIN 288 301 NUCLE
                                                 Submitted
                                                                                                                                                                                                                            "Isolation of canine p53 cDNA and full length canine p53 protein."; Oncogene 16:1077-1084(1998).
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Carnivora;
MCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD002681; P53; 1
PROSITE; PS00348; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRO
Pfam; PF00870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF071571; AAD34213.1; HSSP; P04637; ITUP.
    SEQUENCE
                                                                      tumors in
                                                                                         Watari T., Hasagawa
"Aberrations of p53
                                                                                                                                      Setoguchi A., Sakai
                                                                                                                                                         TISSUE=Spleen;
                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                     TISSUE=Leukocyte;
MEDLINE=98178696;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                     Veldhoen
                                                                                                                                                                                                                                                                        Veldhoen N., Milner J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
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148; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
    S
S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKSKTASSAEEDNNEVYTLQIRGRKRYEMLKKINDGLDLLENKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKRRS-----PDDELLYLPVRGRETYEMLLKIKESLELMQYLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERAQYFEHPHTKRQSVTVPYEPPQLGSEFTTILLSFMCNSSCMGGMNRRPILTILTLETQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEVILGKDPPMGAVLRATAIYKKTEHVAEVVRRCPHHQ-----NEDSAEHRSHLIRMEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPPSRDGANSSSPTVPVTTDYPGEYGFKLRFQKSGTAKSVTSTYSEILNKLYCQLAKTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGIVLGRRCFEVRVCACPGRDRKTEETNSTKMQ-----
                                                                         the
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                                               (DEC-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366
367
    25-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                      dog
                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P53;
                                                                                                                                                                                                                                                                                                                        PubMed=9519881;
    FROM
                                                                                  T., Okuda M., Mir
A., Tsujimoto H.;
tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.8%;
51.9%;
    z
                                                                                                               Okuda M., Minehata K., Tsujimoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Mismatches
                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 745; DB 1;
Pred. No. 1.3e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY SIMILARITY)
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                                                                                         various
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                                               databases
                                                                                                                                    Yazawa M.,
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                                                                                                                                      Ishizaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P04637; 10LG.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF060514; AAC16909.1; -.
EMBL; AB020761; BAA78379.1; -.
EMBL; S77819; AAB42022.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression.
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                      193
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                                                                                                                                                       VSSPPPPNTCVRAMAIYKKSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAK
LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                              YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                          VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                                 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                     ENNAQTQFSEPQYTNL----GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                   YLDDRNTFRHSVVVPYEPPEVGSDYTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNV
                                                                                                                                                                                                                                                                PL----SSSVPSPKTYPGTYGFRLGFLHSGTAKSVTWTYSPLLNKLFCQLAKTCPVQLW
                                                                                                                                                                                                                                                                                                                                                                    ENNVLSSELCPAVDELLLPESVVNWLDE-----DSDDAPRMP--ATSAPTAPGP--APSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 739; DB
Pred. No. 4e-49
52; Mismatches
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MEES -> MQEP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (FOTENTIAL).
PHOSPHORYLATION (BY PRPK) (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLIGOMERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102;
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P79820; Q9PSU7; Q9PSU8;
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor;
TP53 OR P53.
                                                                                                                                                                                                                                                                                                               EMBL; U57306; AAC60146.1; -.
EMBL; AF003949; AAD01195.1; -.
EMBL; AF003949; AAD01196.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H. "Isolation of cDNAs encoding the p53 tumor suppressor ge Japanese Medaka (Oryzias latipes).";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krause M.K., Rhodes L.D., van Beneden R.J.;
"Cloning of the p53 tumor suppressor gene from (Oryzlas latipes) and evaluation of mutational exposed fish.";
Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
DOMAIN 1 48 TRANSCRIPTION ACTIVATION (ACIDIC).
DNA_BIND 87 273 BY SIMILARITY.
                                                                                                                             PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                             Pfam; PF00870; P53;
                                                                                                                                                                                                                                                    InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 189:101-106(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression (By similarity).
SUBUNIT: BINGS DNA as a homotetramer (By
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAX and FAS antigen expression, or by
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                                                                                                                                                                                                                                                                                        AF003950; AAD01196.1; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLDGEYFTLQIRGRERYEMFRNLNEALEL 338
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                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97376996; PubMed-9233767; Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.; "Partial characterization of the woodchuck tumor suppressor, its interaction with woodchuck hepatitis virus X antigen in hepatocarcinogenesis."; Oncogene 15:327-336(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O36006;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marmota monax (Woodchuck).
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                                                                                            SUBUNIT: Binds DNA as a homotetramer SUBCELLULAR LOCATION: Nuclear. DISEASE: p53 is found in increased am of transformed cells. p53 is frequent in many types of cancer.
                                                                                                                                                                                                                                    growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation on the process of Bcl-2 and FAS antigen expression, or by repression of Bcl-2
                                                                        in many types of cancer.
SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                                                     expression
                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Acts as a tumor suppressor in many tumor types;
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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thi; Sciuridae; Sciurinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ001022; CAA04478.1; HSSP; P04637; 1TUP. InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.4%; Score 736.5; DB 1 al Similarity 41.5%; pred. No. 6.5e-49; 159; Conservative 63: Minmachian 1
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                                                                                                                  366 YLKSKKGQSTSRHKKIIFKREGP 388
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Phosphorylation; Apoptosis.

44 TRANSCRIPTION ACTIVATION (ACIDIC).

290 BY SIMILARITY.
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Scoring table:
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Perfect score:
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Listing first 45 summaries
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 SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_inverteb;
6: sp_mammal:*
5: sp_mhc:*
8: sp_organel:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_vtrus:*
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14: sp_urclass
15: sp_vtrus:
16: sp_bacteri
17: sp_archeap
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Gapop 10.0 , Gapext 0.5
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2082
1 MLYLENNAQTQFSEPQYTNL.....PKQSDVFFRHSKPPNRSVYP 393
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	. 10	9	8	7	6	u	4	w	2	1	Result No.
1873	1873	1882	1882	1884	1884	1884	1884	1884	1938	1973	1973	2009	2011	2039	2082	Score
90.0	90.0	90.4	90.4	90.5	90.5	90.5	90.5	90.5	93.1	94.8	94.8	96.5	96.6	97.9	100.0	Query Match
586	461	586	461	586	586	461	461	416	483	487	470	389	487	393	393	Length
11	11	11	11	4	4	4	4	4	11	11	11	11	4	11	4	DB
Q99JE2	Q99JD6	089097	Q9QWY9	Q9P1B4	Q9UBV9	Q9UP26	Q9P1B5	Q9P1B6	088897	Q99JE0	Q99JE1	668880	Q9H3D2	Q99JD9	075922	ID
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4444	38 41 11	34 35 37	327	26 27 28 30	22 23 24 25	17 18 19 20
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Q8tdy6 homo sapien Q8tdy6 homo sapien Q96kr0 homo sapien Q9cu77 mus musculu	mus mus bark	Q8jfe3 brachydanio Q8jhz6 brachydanio Q8c826 mus musculu Q9h3p8 homo sapien	rattus xenopus brachyd	mus gall ratt ratt	0	Q9up74 homo sapien Q75080 homo sapien Q9nph7 homo sapien Q9plb7 homo sapien

ALIGNMENTS

6666668888	RA RA RA	RR	RESULT 075922 ID 0 AC 0 DT 0 DT 0 DT 0 DT 0
SEQUENCE FROM N.A. Hagiwara K., McMenamin M.G., Harris C.G.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES OF ERROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.	SEQUENCE FROM N.A. MEDLINE-98448095; Pubmed-9774969; Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.; "p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities."; Mol. Cell 2:305-316(1998).	P63. Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Leukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=20388515; PubMed=10935472; Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S., YOkota J., "Mutation and expression of the p51 gene in human lung cancer."; Meoplasia 1:71-79(1999).	LT 1 O75922 PRELIMINARY; PRT; 393 AA. O75922; O1-NOV-1998 (TrEMBLrel. 08, Created) O1-NOV-1998 (TrEMBLrel. 08, Last sequence update) O1-OCT-2002 (TrEMBLrel. 22, Last annotation update) P51 isoform DELNGAMMA (DN P63 gamma) (Cellular tumor antigen

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
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SIMILARTY: BELONGS TO THE P53 FAMILY.

L; AF075429; AAC62634.1;
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AF116759; AAF43490.1;
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                                                                                                               CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
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                                                                                                CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
                                                                                                                                                                           SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSA
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                                                                                                                                                           SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
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                PRELIMINARY;
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LAR LOCATION: NUCLEAR (BY SIMILARITY).
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InterPro; IPRO02117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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FEBS Lett. 501:121-126(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
DN KET gamma protein (Ce
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification and tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: ACTS AS À TUMÓR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTRANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APODTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
                                                                                                                                                                                                                                                                                                                                                                      TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
                                                                                                                                                                                                                                                                                         MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                          SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSA
                                                            SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLLQKHLLSA
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Pred. No. 2.7e
1; Mismatches
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ches 7;
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                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98448095; PubMed-9774969; Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch 'Nandrews N.C., Caput D., McGen F.; P63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activity. Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                   PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osada M., Ohba M., Kawahara C., Ishioka C., Ikawa Y., Nimura Y., Nakagawara A., Obinata "Cloning and functional analysis of human pt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Skeletal muscle;
MEDLINE-98324755; PubMed-9662378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neoplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 40-487 MEDLINE=20388515; I
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Nat. Med. 4:839-843(1998).
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Submitted (JAN-1999) to t
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SIMILARITY: BELONGS TO
                                                                                                                                                                                    AF116770; AAF43486.1
AF116756; AAF43486.1
AF116757; AAF43486.1
AF116759; AAF43486.1
AF116750; AAF43486.1
AF116762; AAF43486.1
AF116762; AAF43486.1
                                                                                                                                                                                                                                                                                                                                                                                                                                               AF124528;
AF124529;
                                                                          PF00870;
                                                                                                             P04637;
                                                                                                                                AF116765;
                                                                                                                                                 AF116764; AAF43486
                                                                                                                                                                                                                                                                                                                                                                                                                               AF124531;
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-2001 (TrEMBLrel. 16, Last seque
-2002 (TrEMBLrel. 22, Last annot
gamma (P51 isoform TAP63GAMMA).
   protein
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                                                                          IPR002117; P53.
0870; P53; 1.
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BAA32592.
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PubMed=10935472;
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p51, which structurally
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Best Local
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088899;
01-NOV-1998
01-NOV-1998
01-OCT-2002
  EMBL;
HSSP;
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                     TRP63.
                                                                                                                                                                                                                                                                                                                                                                                               DN p63 gamma
                                                                                                                                                                                                                          transactivating, death-inducing, and Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                           MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Gillett E., Fleming
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
EXPRESSION (BY SIMILARITY).

SUBUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN I
TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OF
MANY TYPES OF CANCER (BY SIMILARITY).

SIMILARITY: BELONGS TO THE P53 FAMILY.

SIMILARITY: ACC62642.1; -.

SP; P04637; 1YCS.
                                                                                                                 FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTRACCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375
                                                                                                                                                                                                                                      a p53 homolog at 3q27-29, encodes multiple products with activating, death inducing, and dominant-negative activit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                             Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KQSDVFFRHSKPPNRSVYP
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Rodentia;
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Pred. No. 1.1e-171;
                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local S
Matches 382
                                                                                                                                                                                                                                                     Q99JE1 PRELIMINARY;
Q99JE1;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-CCT-2002 (TrEMBLrel. 2
                                                                                                                               STRAIN=Wistar; TISSUE-Tongue; MEDLINE-21363378; PubMed-11470269; Bamberger C., Schmale H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear Phosphorylation; Transcription; Transcription regulation.
SEQUENCE 389 AA; 43970 MW; FE6B4A859C5F00BB CRC64;
        Interpro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
                                                   -i- SUBCELLULAR LOCATION: NUCLE

-i- SIMILARITY: BELONGS TO THE

EMBL; AJ277448; CAC37100.1; -.

HSSP; P04637; IYCS.
                                                                                                variants.";
FEBS Lett. 501:121-126(2001).
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                      "Identification and tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1330810; Trp63.
InterPro; IPR002117; P53.
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                                                                                                                                                                                                                                                                                                                                                                    CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIIVTLETRDGQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           LGRRCFEARICACPGRDRKADEDSIRKQQVSDSAKNGDA----FRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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17,
22,
                                                                                      NUCLEAR
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Last annotation update)
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Pred. No. 1.3e-171;
0; Mismatches 7;
                                                                                                                                                                                               Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                      SIMILARITY)
                                                                                                                      of
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                                                                                                                      novel KET/p63
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
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Best Local
Matches 37
                     Query Match
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Best Local
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099JE0;
01-JUN-2001
01-JUN-2001
01-OCT-2002
                                                 PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
                                                                                    InterPro; IPR002117; P53. Pfam; PF00870; P53; 1. PRINTE: PF00870; P53; 1.
                                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR (
-!- SIMILARITY: BELONGS TO THE P53
EMBL; AJZ77449; CAC37101.1; --
HSSP; P04637; 1XCS
                                                                                                                                                                                  STRAIN-Wistar; TISSUE-Tongue; MEDLINE-21363378; PubMed-11470269; Bamberger C., Schmale H.;
                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                          Nuclear protein. SEQUENCE 487 F
                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                       FEBS
                                                                                                                                                                variants.";
                                                                                                                                                                         Bamberger C., Schmale H.;
"Identification and tissue distribution
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  372;
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           Similarity
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                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      KQSDVFFRHSKPPNRSVYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                           ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRDRKADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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98.2%;
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Pred. No. 2.8e
0; Mismatches
Score 1973; DB 11;
Pred. No. 2.9e-168;
0; Mismatches 7;
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                                                                                                                                                                                                                                              Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                          A688F392F32B3039
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                                                                                                                                  (BY SIMILARITY)
FAMILY.
                                                                                                                                                                                                                                                                                                                                         487
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es 7;
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                                                                                                                                                                          novel KET/p63
                                          CRC64;
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                     Length
  Indels
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                                                                                                                                                                                                                                                Murinae;
                      487;
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314 404

us-09-538-106-18.rspt

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Neoplasia 1:71-79(1999).

CIPCUTON: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CROWTH ARREST OR APOPTOSIS INDUCTOR SENSOR THIS PROCESS. ONE OF THE ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE ORD OF THE ACTIVATED GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

CHAPOPTOSIS INDUCTION SEEMS TO BE MEDITATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION (BY SIMILARITY).

CHORDOLOGY.

CHAPTER AND ARREST OF THE PHYSION OF BCL-2 CONDITIONS OF BCL-2 CONDITIONS
                                                                                                                                    ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP 374
                                                                                                                                                                                                                                                                                             TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAM 228
                                    GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                  PYEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPIL1IVTLETRDGOVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mutation and expression of the p51 gene in human lung cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-20388515; PubMed-10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2002 (TrEMBLrel. 22, Last annotation update P51 isoform delNdelta (Cellular tumor antigen p53) Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MANY TYPES OF CANCER (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL, AR116769, AAR43493.1; O'THE D5.
EMBL, AR116759, AAR43493.1; JOINED.
EMBL, AR116760, AAR43493.1; JOINED.
EMBL, AR116761, AAR43493.1; JOINED.
EMBL, AR116762; AAR43493.1; JOINED.
EMBL, AR116763; AAR43493.1; JOINED.
EMBL, AR116763; AAR43493.1; JOINED.
EMBL, AR116764; AAR43493.1; JOINED.
EMBL, AR116764; AAR43493.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 AA
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                                                                                                                                                                                                                                                                                                                                                                        TQSDVFFRHSNPPNHSVYP 483
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Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
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EMBL; AF116766; AAF43493.1;
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                    75 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 134
                                                                           TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 134
                                                                                                                                                    PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
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74
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MEDLINE-98448005; PubMed-9774969;
Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
Caput D., McKeon F.;
                                                                                                                                                                                                                                                                                                                                                                                                             ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
PQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA1PSN
                                                                                                                                                                                                                                PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                           GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities."; Mol. Cell 2:305-316(1998).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- SIMILARITY: BELONG: TO THE P53 FAMILY.

EMBL; AF075434; AAC62639.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 93.1%; Score 1938; DB 11; 31 Similarity 97.1%; Pred. No. 3.9e-165; 368; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQSDVFFRHSKPPNRSVYP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 TQSDVFFRHSNPPNHSVYP 487
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InterPro; IPR002117; P53.
Pfam; PF00870; P53; IP.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; P0002681; P53; I.
PROSITE; PS00348; P53; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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SEQUENCE 483 1
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Best Local S
Matches 368
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ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
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                                      Nuclear protein
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                                                                                                               Gaps
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| "Mutation and expression of the p51 gene in human lung cancer.";
| Neoplasia 1:11-79(1999).
| Substitution and Location | NUCLEAR (BY SIMILARITY).
| SINGLIARITY: BELONGS TO THE P53 FAMILY.
| EMBL; AF116769; AAF43492.1; JOINED. |
| REMBL; AF116769; AAF43492.1; JOINED. |
| REMBL; AF116761; AAF43492.1; JOINED. |
| REMBL; AF116762; AAF43492.1; JOINED. |
| REMBL; AF116763; AAF43492.1; JOINED. |
| REMBL; AF116764; AAF43492.1; JOINED. |
| REMBL; AF116765 | AAF43492.1; JOINED. |
| REMBL; AAF43492.1; JOINED. |
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Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein; Phosphorylation; Transcription; Transcription regulation. SEQUENCE 416 AA; 46589 WW; A5974A14B25E3118 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
P51 isoform delNubeta.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.
                                                                                                             16;
                                                                           Length 416;
                                                                                                            Indels
                                                                       90.5%; Score 1884; DB 4;
93.3%; Pred. No. 2.2e-160;
iive 3; Mismatches 7;
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MEDLINE=20388515; PubMed=10935472;
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EMBL; AF116766; AAF43492.1; JOINED.
EMBL; AF116767; AAF43492.1; JOINED.
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Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
                                                                                        Best Local Similarity 93.3
Matches 361; Conservative
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                                                                                                                                                                                              TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
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                                                                               Gaps
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Yang.A., Raghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                           16;
                                      Length 461;
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68B63547B81C1B05 CRC64;
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Last annotation update)
                                Score 1884; DB 4;
Pred. No. 2.6e-160;
3; Mismatches 7;
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-OCT-2002 (TrEMBLrel. 22, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
MM;
                                  / Match 90.5%;
Local Similarity 93.3%;
les 361; Conservative
461 AA; 51305
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61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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01-OCT-2000 (TTEMBLrel. 15, Created)
01-OCT-2000 (TTEMBLrel. 22, Last sequence update)
01-OCT-2002 (TTEMBLrel. 22, Last annotation update)
P51 isoform delNalpha.
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                             Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                        2E2F92ABF1AF8629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  90.5%; Score 1884; DB 4; 93.3%; Pred. No. 3.5e-160; iive 3; Mismatches 7;
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InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; I.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; I.
SMART; SM00454; SAM; I.
PROSITE; PS00348; P53; I.
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Matches 361; Conservative
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                   SEQUENCE FROM N.A.
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SEQUENCE 586 A
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                                                                                                                                                                                                                         1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                       LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McReon F.;
"p63, a p53 homolog at 3427-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                               Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Dellavalle R.P., Targoff I.N., Kaufman K.M., Chorzelski T.P.,
Jablonska S.;
                                                                                                                                                                                               16;
                                                                                                                                                               90.5%; Score 1884; DB 4; Length 461; 93.3%; Pred. No. 2.6e-160; Live 3; Mismatches 7; Indels 10
                                                                                                                                     461 AA; 51404 MW; 68B63547A46C1B05 CRC64;
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InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00336; P535UPPRESSR.
PRODOM; PD0002681; P53; 1.
PROSITE; PS00348; P53; 1.
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Best Local Similarity 93.33
Matches 361; Conservative
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SEQUENCE FROM N.A.
                                                                                                                       Nuclear protein.
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                                                               | Mutation and expression of the p51 gene in human lung cancer.";
| Neoplasia 1:71-79(1999).
| Neoplasia 1:71-79(1999).
| SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
| SIMECLIARITY: BELONGS TO THE P53 FAMILY.
| REMBL; AFI16758; AAF43491.1; JOINED.
| REMBL; AFI16759; AAF43491.1; JOINED.
| REMBL; AFI16761; AAF43491.1; JOINED.
| REMBL; AFI16762; AAF43491.1; JOINED.
| REMBL; AFI16763; AAF43491.1; JOINED.
| REMBL; AFI16764; AAF43491.1; JOINED.
| REMBL; AFI16764; AAF43491.1; JOINED.
| REMBL; AFI16765; AAF43491.1; JOINED.
                     ŠEČUENCE FROM N.A.
BEDLINE-20388515; Pubmed-10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                              90.5%; Score 1884; DB 4; Length 586; 93.3%; Pred. No. 3.5e-160; ive 3; Mismatches 7; Indels 1
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PRINTS; PR00366; P53SUPPRESSR.
ProDom; P0002681; P53; 1.
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AF116768; AAF43491.1;
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InterPro; IPR001660; SAM.
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Wataryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                          MEDLINE-98448095; PubWed-9774969;
Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews
Caput D., McKeon F.;
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93.0%; Pred. No. 3.9e-160;
iive 3; Mismatches 8;
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01-NOV-1998 (TERMBLrel. 08
01-0CT-2002 (TERMBLrel. 23
DN P63 alpha.
TRP63 OR P73H.
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Mus musculus (Mouse)
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T "A second p53-related protein, p71L, with high homology to Biochem. Biophys. Res. Commun. 248:603-607(1998).

C -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

C -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

R EMBL; AF075439; AAC62644.1; -.

R EMBL; AF075439; AAC62644.1; -.

R EMBL; AF075439; AAC62644.1; -.

R HSSP, P04637; 1YCS.

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R HSSP, P04637; 1YCS.

R MGD; MGI:1330810; Trp63.

R InterPro; IPR001160; SAM.

R Pfam; PF00870; P53; 1.
Q99JD6;
01-JUN-2001
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DN KET beta
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ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
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SEQUENCE FROM N.A.
MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Gillett E., Fleming M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Yammalia: Entheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00386; P53SUPPRESSR. Probom; PD002681; P53; 1. PROSITE; P800348; P53; 1. Nuclear protein. SEQUENCE 461 AA; 51398 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-Wistar; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification and tissue distribution of variants.";
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: NI
-1- SIMILARITY: BELONGS TO 'EMBL; AJ277453; CAC37105.1; HSSP; P04637; 1YCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21363378; PubMed=11470269;
                                                                                                                                                                                                                                                                                                                                          Match
Local (
                                                            361
                                                                                301
                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                     protein.
E 461 AA; 51398 MW;
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                      TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                                                                                                                                                                                    MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                    CFRNELVEPRRETPKQSDVFFRHSKPP
                                                                                          SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLLQKHLLSA
                                                                                                                                                                                                                                                TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                                                                                                                                                                         MLYLESNAQTQFSEPQYTNLGLLNGMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501:121-126(2001).
                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Tongue
       7,
                                        QTSMQSQSSYGNSSPP
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           2003,
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                                                                                                                                                                                                                                                                                                                                         Score 1873;
Pred. No. 2
           09:51:44
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                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY). FAMILY.
                                         371
                                                                                                                                                                                                                                                                                                                               2.5e-159;
nes 9;
                                                                                                                                                                                                                                                                                                                                                     BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel KET/p63 splice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                    120
                                                                                                  360
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